

## SEQUENCE LISTING

- <110> Genentech, Inc.  
Ashkenazi, Avi  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, A.  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth, J.  
Kljavin, Ivar J.  
Mather, Jennie P.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
<141> 2000-09-18
- <150> PCT/US00/04414  
<151> 2000-02-22
- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
<151> 1999-07-26
- <150> US 60/146,222  
<151> 1999-07-28
- <150> PCT/US99/20594  
<151> 1999-09-08
- <150> PCT/US99/20944  
<151> 1999-09-13

<150> PCT/US99/21090  
<151> 1999-09-15

<150> PCT/US99/21547  
<151> 1999-09-15

<150> PCT/US99/23089  
<151> 1999-10-05

<150> PCT/US99/28214  
<151> 1999-11-29

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28564  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/30911  
<151> 1999-12-20

<150> PCT/US99/30999  
<151> 1999-12-20

<150> PCT/US00/00219  
<151> 2000-01-05

<160> 423

<210> 1

<211> 1825

<212> DNA

<213> Homo sapiens

<400> 1

```
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60
gaccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120
cccgcagcgc tacccgccat gcgcctgccg cgcggggccg cgetgggggt cctgccgtt 180
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccttg ccaccgggtg 240
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcgggaaca cggcttggga ggaaaagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgcgag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgcagg aggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggt 540
cccgactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg gtaccagggc 660
```

```

ccgctgtgca ctgactgcat ggacggctac ttcagctcgc tccggaacga gacccacagc 720
atctgcacag cctgtgacga gtcctgcaag acgtgctcgg goctgaccaa cagagactgc 780
ggcgagtgtg aagtgggctg ggtgctggac gagggcgccct gtgtggatgt ggacgagtgt 840
gcgggccgagc cgcctccctg cagcgctgcg cagttctgta agaacgcaa cggctcctac 900
acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc aggaaactgt 960
aaagagtgtg tctctggcta cgcgaggag cagcgacagt gtgcagatgt ggacgagtgc 1020
tcactagcag aaaaaacctg tgtgaggaaa aacgaaaact gctacaatac tccagggagc 1080
taogtctgtg tgtgtcctga cggcttcgaa gaaacggaag atgcctgtgt gccgcccgcga 1140
gaggtctgaag ccacagaagg agaaagccc acacagctgc cctcccgcga agacctgtaa 1200
tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat gtggccctga 1260
ggatgccgtc tcctgcagtg gacagcggcg gggagaggct goctgctctc taacggttga 1320
ttctcatttg tcccttaaac agctgcattt cttggttgtt cttaaacaga cttgtatatt 1380
ttgatacagt tctttgtaat aaaattgacc attgtaggta atcaggagga aaaaaaaaaa 1440
aaaaaaaaaa aaagggcggc cgcgactcta gactcgacct gcagaagctt ggccgccatg 1500
gcccacttg tttattgcag cttataatgg ttacaaataa agcaatagca tcacaaattt 1560
cacaaataaa gcattttttt cactgcattc tagttgtggt ttgtccaaac tcatcaatgt 1620
atcttatcat gtctggatcg ggaattaatt cggcgcagca ccatggcctg aaataacctc 1680
tgaaagagga acttggttag gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg 1740
tcagttaggg tgtggaaagt ccccaggctc ccagcaggc agaagtatgc aagcatgcat 1800
ctcaattagt cagcaacca gttttt 1825

```

<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1                      5                      10                      15

```

```

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
                20                      25                      30

```

```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
    35                      40                      45

```

```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
    50                      55                      60

```

```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
    65                      70                      75                      80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
                85                      90                      95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
    100                      105                      110

```

```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
    115                      120                      125

```

```

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
    130                      135                      140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
 325 330 335  
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp  
 340 345 350  
 Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

cagggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatacctc tagagatccc 60  
 tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120  
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gaggcagcatg gcccgaggga 240

```

gcgccttccc tgccgcgcgc ctctggctct ggagcactct cctgtgcctg ctggcactgc 300
gggcggaggg cgggcgcgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360
caagagtact cataggattt gaagaagata tcttgattgt ttcagagggg aaaatggcac 420
cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480
attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
ccttgcgctc cctggataaa ggcacatcag cagatccaac cgtcaatgtc cctctgctgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtcct ggaaaacagg 660
atgggggtgg agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tgcccaggcg 780
ggtgccgaaa tggaggcttt tgtaatgaaa gacgcactct cgagtgtcct gatgggttcc 840
acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900
tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcttt aatggaggga cctgtttcta ccctggaaaa tgtatttgcc 1020
ctccaggact agagggagag cagtgtgaaa tcagcaaattg cccacaaccc tgtcgaaatg 1080
gaggtaaatg cattggtaaa agcaaattgta agtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200
aatgccaatg tcaagaagggt tggcatggaa gacactgcaa taaaagggtac gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgcct tcacttaaaa 1320
aggccgagga gcggcgggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380
aaacgtttta agttacacca agttcatagc ctttgttaac ctttcatgtg ttgaatgttc 1440
aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagctga tatttactct tctttttaag ttttctaagt acgtctgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcagggtta 1620
aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgtctgg 1680
gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttactactgt gtagtggcat 1920
ttaaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980
gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctottac ctaataaaca 2040
ttttatactg tttgtatgta taaaataaag gtgctgcttt agttttttgg aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgc gactctagag tcgacctgca 2160
gaagcttggc cgccatggcc caacttgttt attgcagctt ataatg 2206

```

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
 1             5             10             15

```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20             25             30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
      35             40             45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
      50             55             60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

```

65		70		75		80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln						
	85		90		95	
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly						
	100		105		110	
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro						
	115		120		125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln						
	130		135		140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu						
	145		150		155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr						
	165		170		175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys						
	180		185		190	
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His						
	195		200		205	
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys						
	210		215		220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn						
	225		230		235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys						
	245		250		255	
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln						
	260		265		270	
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys						
	275		280		285	
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu						
	290		295		300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys						
	305		310		315	320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His						
	325		330		335	
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala						
	340		345		350	

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
           355                                  360                                  365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp  
       370                                  375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 5

agggagcacg gacagtgtgc agatgtggac gagtgtcac tagca

45

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 6

agagtgtatc tctggctacg c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 7

taagtccggc acattacagg tc

22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 8

cccacgatgt atgaatggtg gacttttgtt gactcctggt ttctgcac

49

<210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 9  
 aaagacgcat ctgcgagtgt cc

22

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 10  
 tgctgatttc acactgctct ccc

23

<210> 11  
 <211> 2197  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60  
 ggccccagcc cacaccttca ccagggccca ggagccacca tgtggcgatg tccactgggg 120  
 ctactgctgt tgctgccgct ggctggccac ttggctctgg gtgcccagca gggtcgtggg 180  
 cgccggggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccgggtac 240  
 tgccaggagc aggacctgtg ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300  
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360  
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420  
 ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480  
 caggagaaca ggcagtggca tgggtggatcc agacatgate aaagccatca accagggcaa 540  
 ctatggctgg caggctggga accacagcgc cttctggggc atgaccctgg atgagggcat 600  
 tcgctaccgc ctgggcacca tccgccatc ttctcggtc atgaacatgc atgaaattta 660  
 tacagtgtgt aaccacagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720  
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780  
 agcagctgtg gcatccgac gtgtctcaat ccattctctg ggacacatga cgcctgtcct 840  
 gtcgcccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtggg 900  
 tctcgatggg gcctggtggg tctgcgtcg ccgaggggtg gtgtctgacc actgctacct 960  
 cttctcgggc cgtgaacgag acgaggctgg ccttgccccc cctgtatga tgcacagccg 1020  
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080  
 caatgacatc taccaggtca ctctgtcta ccgcctcggc tccaacgaca aggagatcat 1140  
 gaaggagctg atggagaatg gccctgtcca agccctcatg gaggtgcatg aggacttctt 1200  
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260  
 ccgccggcat gggacccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

```

tggaaggacg ctcaaatact ggactgcggc caactcctgg ggcccagcct ggggcgagag 1380
gggccacttc cgcacgtgc gcggcgtaa tgagtgcgac atcgagagct tcgtgctggg 1440
cgtctggggc cgcgtgggca tggaggacat gggcatcac tgaggctgcg ggcaccacgc 1500
ggggtcgggc ctgggatcca ggctaagggc cggcggaaga ggcccgaatg gggcggtgac 1560
cccagcctcg cccgacagag cccggggcgc aggcgggcgc caggcgcta atcccggcgc 1620
gggttcgct gacgcagcgc cccgcctggg agccgcgggc aggcgagact ggcggagccc 1680
ccagacctcc cagtggggac ggggcagggc ctggcctggg aagagcacag ctgcagatcc 1740
caggcctctg gcgccccac tcaagactac caaagccagg acacctcaag tctccagccc 1800
caatacccca cccaatccc gtattctttt tttttttttt ttagacaggg tcttgctccg 1860
ttggccaggt tggagtgcag tggcccatca gggctcactg taacctccga ctctggggtt 1920
caagtgacct tcccacctca gcctctcaag tagctgggac tacaggtgca ccaccacacc 1980
tggctaattt ttgtattttt tgtaaagagg ggggtctcac tgtgttgccc aggtggttt 2040
cgaactcctg ggctcaagcg gtccacctgc ctccgcctcc caaagtgtg ggattgcagg 2100
catgagccac tgcaccacgc cctgtattct tattcttcag atatttattt ttcttttcac 2160
tgttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

```

<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly
 1              5              10              15

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
      20              25              30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35              40              45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50              55              60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65              70              75              80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85              90              95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100             105             110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115             120             125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130             135             140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145             150             155             160

His Asp Pro Gly

```

<210> 13  
 <211> 533  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (33)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (80)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (94)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (144)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (188)  
 <223> a, t, c or g

<400> 13  
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcgtt gtctcaaatac 60  
 caattctctt gggacacatn acgcctgtcc tttngcccca gaacctgctg tcttgtacac 120  
 ccaccagcag cagggctgcc gcgntgggcg tctcgatggg gcctgggtgg tcttgcgtcg 180  
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240  
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300  
 tgcccaactgc cccaacagct atgttaataa caatgacatc taccaggtea ctctgtcta 360  
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420  
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480  
 gccagtgagc cttgggaggc cagagagata ccgccggcat gggacccact cag 533

<210> 14  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcggatatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcactgccc tgetgtgcta 60  
ctcctgcaaa gcccagggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120  
gggggagcag tgctggaccg cgcgcataccg cgcagttggc ctctgaccg tcatcagcaa 180  
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240  
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300  
cgccatcctt gcgtgctcc ctgcaactcg cctgctgctc tggggacccg gccagctata 360  
ggctctgggg ggccccgctg cagccacac tgggtgtggg gccccaggcc tctgtgccac 420  
tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480  
gtctgaccat gtatgtctgc acccctgtcc cccaccctga cctcccatg gccctctcca 540  
ggactccac ccggcagatc agctctagt acacagatcc gcctgcagat ggccccctcca 600  
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660  
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc caggctctgg 720  
ccgtggtgtc ccccgacccc agcaggggac aggcactcag gagggcccag taaaggctga 780  
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840  
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900  
aatggcagcc tgagcacagc gtaggcctt aataaacacc tgttgataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcttgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

```

cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgcccc acctcactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcacgg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcggaagc ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttcagaa 420
cgcccggcac gagggtggtt tcatggcctt cacgcggcag gggcgcccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca ctcatcaag cgctctacc aaggccagct 540
gcccttccc aaccacgccg agaagcagaa gcagttcgag tttgtgggt ccgccccac 600
ccgcccggacc aagcgcacac ggcggcccca gcccctcag tagtctggga ggcagggggc 660
agcagcccct gggccgcctc cccaccctt tccctctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgaggga ggacctgag ggccgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcccc aggggcggct ggcacagtgc ccccttccc 840
gacgggtggc aggccttggg gaggaactga gtgtcaccct gatctcaggc caccagcctc 900
tgccggcctc ccagccgggc tctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctgagtctgc 1020
ccccagcccc caaactcctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
acgacccagg cctgcacccc accccaact cccagccccg gaataaaacc attttcttgc 1200

```

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gcc

24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
 gcggatctgc cgctgctca nctggtcggt catggcgccc t

41

<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 acttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60  
 aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120  
 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180  
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240  
 tatttttattt ccgtacttca gaaatgggac tacagaccac aaagtggccc agccatgggg 300  
 cttttttcct gaagtcttggt cttatcattt ccctgggggt ctactcacag gtgtccaaac 360  
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
 gcttgacctc agtgccctctt gggatcccg agggcgtaac cgtactctac ctccacaaca 480  
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtgc gtgcacacgg 540  
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ctttcccaag aatgtcagag 600  
 ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gccagctct 660  
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720  
 gggccttcog ggaggctatt agcctcaaat tgttggtttt gtctaagaat cacctgagca 780  
 gtgtgcctgt tgggcttcct gtggacttgc aagagctgag agtggatgaa aatcgaattg 840  
 ctgtcatata cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900  
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960  
 aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccaggtacgc 1020  
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aaggggtttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcattctctca 1260
acgtgcgggg tttcatgtgc caaggtcctg aacaagtcgg ggggatggcc gtcagggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgacccccgg cctgcctctc ttcaccccag 1380
ccccaagtac agcttctccg accactcagc ctcccaccct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctgggtct ctctcttcac cgtgatggca taaaaactca 1620
catgggtgaa aatggggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttggt 1740
tagtgccact ggatgctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catgggtctc ccttttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggg ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcgaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaagggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcaactgcat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggtg tactatataa 2400
tgggatttaa aaaaagtgc tcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt
2479

```

&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
  1                      5                      10                      15

```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
          20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
          35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
          50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
          65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
          85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
          100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
          115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

				405						410					415	
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val	
			420					425					430			
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met	
		435					440					445				
Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly	
	450					455					460					
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu	
465					470					475					480	
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu	
				485					490					495		
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala	
			500					505					510			
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser	
		515					520					525				
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala	
	530					535					540					
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser	
545					550					555					560	
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys	
				565					570					575		
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly	
			580					585					590			
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln	
		595					600					605				
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu	
	610					615					620					
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His	
625					630					635					640	
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu	
				645					650					655		
His	Cys	His	Thr													
			660													

<210> 29  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggctctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcgggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctccccc gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

gaggaagacc cgggtggtg cgccctgcc tcgcttccca ggcgcggcg gctgcagcct 180  
 tgccctctt gctcgcttg aaaatggaaa agatgctcgc aggtctgtt ctgctgatcc 240  
 tcggacagat cgtcctctc cctgccgagg ccaggagcg gtcacgtggg aggtccatct 300  
 ctaggggcag acacgctcgg acccacccgc agacggccct tctggagagt tectgtgaga 360  
 acaagcgggc agacctggtt ttcattctg acagctctcg cagtgtcaac acccatgact 420  
 atgcaaaggt caaggagtgc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480  
 tcacccgagt gggcctgctc caatatggca gcactgtcaa gaatgagttc tccctcaaga 540  
 ccttcaagag gaagtccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600  
 gcacatgac tgggtggcc atccagtatg ccctgaacat cgcattctca gaagcagagg 660  
 gggcccgcc cctgaggag aatgtgccac gggtcataat gatcgtgaca gatgggagag 720  
 ctacaggactc cgtggccgag gtggctgcta aggcacggga cacgggcac ctaatctttg 780  
 ccattggtgt gggccaggta gacttcaaca ccttgaagtc cattgggagt gagccccatg 840  
 aggaccatgt ctctctgtg gccaatctca gccagattga gacgtgacc tccgtgttcc 900  
 agaagaagtt gtgcacggcc cacatgtgca gcaccctgga gcataactgt gccacttct 960  
 gcatcaacat ccctggctca tacgtctgca ggtgcaaaca aggtacatt ctcaactcgg 1020  
 atcagacgac ttgcagaatc caggatctgt gtgccatgga ggaccacaac tgtgagcagc 1080  
 tctgtgtgaa tgtgccgggc tcttctgtc gccagtgtca cagtggctac gccctggctg 1140  
 aggatgggaa gaggtgtgtg gctgtggact actgtgcctc agaaaaccac ggatgtgaac 1200  
 atgagtgtgt aaatgctgat ggctcctacc tttgccagt ccatgaagga tttgctctta 1260  
 acccagatga aaaaacgtgc acaaggatca actactgtgc actgaacaaa ccgggtctgtg 1320  
 agcatgagt cgtcaacatg gaggagagct actactgccg ctgccaccgt ggctacactc 1380  
 tggaccccaa tggcaaaaacc tgcagccgag tggaccactg tgcacagcag gaccatggt 1440  
 gtgagcagct gtgtctgaac acggaggatt ccttctgtc ccagtgtca gaaggcttcc 1500  
 tcatcaacga ggacctcaag acctgtctcc ggtggatta ctgctgtctg agtgaccatg 1560  
 gttgtgaata ctctgtgtc aacatggaca gatccttgc ctgtcagtgt cctgagggac 1620  
 acgtgtccg cagcgatggg aagacgtgtg caaaattgga ctctgtgtc ctgggggacc 1680  
 acggttgtga acattctgt gtaagcagtg aagattcgtt tgtgtgccag tgctttgaag 1740  
 gttatatact ccgtgaagat ggaaaaacct gcagaaggaa agatgtctgc caagctatag 1800  
 accatggctg tgaacacatt tgtgtgaaca gtgacgactc atacacgtgc gagtgttg 1860  
 agggattccg gctcgtgag gatgggaaac gctgccgaag gaaggatgtc tgcaaatcaa 1920  
 cccaccatgg ctgcgaacac atttgtgtta ataattggaa ttctacatc tgcaaatgct 1980  
 cagagggatt tgttctagct gaggacggaa gacggtgcaa gaaatgcact gaaggcccaa 2040  
 ttgacctggt ctttgtgat gatggatcca agagtcttg agaagagaat tttgaggctg 2100  
 tgaagcagtt tgtcactgga attatagatt ccttgacaat tcccccaaa gccgtctgag 2160  
 tggggctgct ccagtattcc acacaggtcc acacagagtt cactctgaga aacttcaact 2220  
 cagccaaaga catgaaaaaa gccgtggccc acatgaaata catgggaaag ggtctatga 2280  
 ctgggctggc cctgaaacac atgtttgaga gaagttttac ccaaggagaa ggggccaggc 2340  
 ccctttccac aagggtgccc agagcagcca ttgtgttcac cgacggacgg gctcaggatg 2400  
 acgtctccga gtgggccagt aaagccaagg ccaatggat cactatgtat gctgttggg 2460  
 taggaaaagc cattgaggag gaactacaag agattgcctc tgagcccaca aacaagcatc 2520  
 tcttctatgc cgaagacttc agcacaatgg atgagataag tgaaaaactc aagaaggca 2580  
 tctgtgaagc tctagaagac tccgatggaa gacaggactc tccagcaggg gaactgcca 2640  
 aaacggtcca acagccaaca gaatctgagc cagtcccat aaatatcaa gacctactt 2700  
 cctgttctaa ttttgagt caacacagat atctgtttga agaagacaat cttttacgg 2760  
 ctacacaaaa gctttccat tcaacaaaac cttcaggaag ccctttggaa gaaaaacacg 2820  
 atcaatgcaa atgtgaaaac cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880  
 aattaacaca gcgttagaa gaaatgacac agagaatgga agccctggaa aatcgctga 2940  
 gatacagatg aagattagaa atcgcgacac atttgtagt attgtatcac ggattacaat 3000  
 gaacgcagt cagagcccca aagctcaggc tattgtttaa tcaataatgt tgtgaagtaa 3060  
 aacaatcagt actgagaaac ctggtttgc acagaacaaa gacaagaagt atacactaac 3120  
 ttgtataaat ttatctagga aaaaaatcct tcagaattct aagatgaatt taccaggtga 3180  
 gaatgaataa gctatgcaag gtattttgt atatactgtg gacacaactt gcttctgcct 3240  
 catcctgcct tagtgtgcaa tctcatttga ctatacgata aagtttgcac agtcttactt 3300

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360  
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggaacaa gttggatttt 3420  
 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
 1 5 10 15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln	Asp Leu Cys Ala	Met Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn	Val Pro Gly Ser	Phe Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
	305	310	315	320		
Val Asp Tyr Cys	Ala Ser Glu Asn	His Gly Cys Glu	His Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
	385	390	395	400		
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
	465	470	475	480		
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Arg Tyr Arg  
915

```
<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35  
gtgaccctgg ttgtgaatac tcc 23

```
<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<400> 36
acagccatgg tctatagctt gg                                     22
```

```
<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

```

ggagccgccc tgggtgtcag cggctcggtt cccgcgcacg ctccggccgt cgcgcagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgcccct gactccgtcc cggccaggga 120
gggcatgat ttcctccccg gggccccctg tgaccaactt gctgcggttt ttgttcctgg 180
ggctgagtgc cctcgcgccc ccctcgcggg ccagctgca actgcacttg ccgccaacc 240
ggttgagggc ggtggagggg ggggaagtgg tgcttcacg gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaag 360
aaaaggagga tcaggtgttg tcctacatca atgggggtcac aacaagcaaa cctggagtat 420
ccttggtcta ctccatgccc tcccgaacc tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg ccctacagc tgcctcgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaacctta gaactcaatg tactggttcc tccagctcct ccactctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660
gtaagccgcg tgtccaatac cagtgggatc ggagcttcc atccttcag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tctccatgg 780
ctggagtcta tgtctgcaag gccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagtgag cacagggcct ggagctgcag tggttgctgg agctgttggt ggtaccctgg 900
ttggactggg gttgctggct gggctggtcc tcttgtaaca ccgcgggggc aaggccctgg 960
aggagccagc caatgatatc aaggaggatg ccattgctcc ccggaccctg ccctggccca 1020
agagctcaga cacaatctcc aagaatggga cccttctctc tgtaacctcc gcacgagccc 1080
tccggccacc ccatggccct ccagggctg gtgcattgac cccacgccc agtctctcca 1140
gccaggccct gcctcacca agactgccc cgacagatgg ggcccacct caaccaatat 1200
cccccatccc tgggtggggt tcttctctg gcttgagccg catgggtgct gtgctgtga 1260
tggtgcctgc ccagagtcaa gctggctctc tggatatgat accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tcctataagg gtcaacctta gcacagaggg ctgagtcatt 1380
ggaaagagtc acactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccaccc acccctgact cctccttatg aagccagctg ctgaaattag 1560
ctactcacca agagtgaggg gcagagactt ccagtcactg agtctcccag gccccttga 1620
tctgtacccc acccctatct aacaccaccc ttggctccca ctccagctcc ctgtattgat 1680
ataacctgtc aggttggtt ggtaggttt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tgttgttttc atttgcaaat ttaaataaag atacataatg 1800
ttgtatgaa aaa

```

1813

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly	Leu Ser Ala Leu Ala Pro	Pro Ser Arg Ala Gln Leu Gln	
	20	25	30
Leu His Leu	Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val		
	35	40	45
Val Leu Pro	Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln		
	50	55	60
Pro Trp Glu	Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys		
	65	70	75 80
Glu Asp Gln	Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro		
	85	90	95
Gly Val Ser	Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg		
	100	105	110
Leu Glu Gly	Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val		
	115	120	125
Asn Val Gln	Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr		
	130	135	140
Leu Glu Leu	Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu		
	145	150	155 160
Gln Gly Val	Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser		
	165	170	175
Pro Arg Ser	Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro		
	180	185	190
Ser Phe Gln	Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser		
	195	200	205
Leu Ser Leu	Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys		
	210	215	220
Lys Ala His	Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu		
	225	230	235 240
Val Ser Thr	Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly		
	245	250	255
Thr Leu Val	Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His		
	260	265	270
Arg Arg Gly	Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp		
	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 370 375 380

Gln Ala Gly Ser Leu Val  
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
 ctgagccgtg ggctgcagtc tcgc 24  
  
 <210> 47

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

&lt;210&gt; 48

&lt;211&gt; 2822

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

```

cgccaccact gcggccaccg ccaatgaaac gcctcccgt cctagtgggt ttttccactt 60
tggtgaattg ttcctatact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120
gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
gcagtaacca agacaggttt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacia gaacaacact atctcagcca aggacacct ttctaactca actcttactg 600
aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900
gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960
acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020
cttcagtaat ttcagtctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080
taacatttac attaatgcat cgaaaggcca cagataggta taggagtcta tgtgcatttt 1140
ggaattactc acctgatacc atgaatggca gctggctctc agagggctgt gagctgacat 1200
actcaaatga gaccacacc tcatgccgt gtaatcacct gacacatttt gcaattttga 1260
tgtcctctgg tccttccatt ggtattaaag attataatat tottacaagg atcactcaac 1320
taggaataat tatttcactg atttgtcttg ccatatgcat ttttaccttc tggttcttca 1380
gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440
ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500
ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560
tacatctcta tctcattggt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620
tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680
acagatatta tggcacaacc aaagtatggt ggcttagcac cgaaaacaac tttatttgga 1740
gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcatca 1800
tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860
taaggctctg tgcaagagga gccctcgctc ttctgttctt tctcggcacc acctggatct 1920
ttggggttct ccatgttgtg cagcatcagc tggttacagc ttacctcttc acagtcagca 1980
atgctttcca ggggatgttc atttttttat tctgtgtgtg tttatctaga aagattcaag 2040
aagaatatta cgatagttgc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
agagaatggt ggataattac aactgcacaa aaataaaaaa tccaagctgt ggatgaccaa 2160

```

```

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtatttttaa 2220
atcagttttt ctgtttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
tagatatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
ggaaagtaat tggtttctca ggagtगतat cactgcaccc aaggaaagat tttctttcta 2400
acacgagaag tatatgaatg tcctgaagga aaccactggc ttgatatttc tgtgactcgt 2460
gttgcccttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
cataagagaa tgaaggggca gaatatcaaa cagtgaaaag ggaatgataa gatgtatttt 2580
gaatgaactg ttttttctgt agactagctg agaaattgtt gacataaaat aaagaattga 2640
agaaacacat tttaccattt tgtgaattgt tctgaactta aatgtccact aaaacaactt 2700
agacttctgt ttgctaaatc tgtttctttt tctaattattc taaaaaaaaa aaaaagggtt 2760
acctccacaa attgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2820
aa
2822

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1              5              10              15

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100              105              110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115              120              125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130              135              140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145              150              155              160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165              170              175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

180					185					190					
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val
		195					200					205			
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys
	210					215					220				
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe
225						230					235				240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys
				245					250					255	
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met
			260					265					270		
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala
		275					280					285			
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser
	290					295					300				
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln
305						310					315				320
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile
				325					330					335	
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys
			340					345					350		
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser
		355					360					365			
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp
	370					375					380				
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser
385						390					395				400
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly
				405					410					415	
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln
			420					425					430		
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr
		435					440					445			
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys
	450					455					460				

```

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465                               470                               475                               480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
                               485                               490                               495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
                               500                               505                               510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
                               515                               520                               525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
                               530                               535                               540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545                               550                               555                               560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
                               565                               570                               575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
                               580                               585                               590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
                               595                               600                               605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610                               615                               620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625                               630                               635                               640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
                               645                               650                               655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
                               660                               665                               670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675                               680                               685

Leu Arg
690

```

&lt;210&gt; 50

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (61)

<223> a, t, c or g

<400> 50

```

tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcattttta tattataaga 120
gtattgggtcc ctttgccttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300
gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tcctctggtc cttccattgg tattaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54  
cgagctcgaa ttaattcg 18

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55  
ggatctcctg agctcagg 18

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56  
cctagttgag tgatccttgt aag 23

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57  
atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt 50

<210> 58  
<211> 2137  
<212> DNA  
<213> Homo sapiens

<400> 58  
gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggctcctctc tcccgcagat ccgaacggcc tgggcgggggt caccgccggt 120

```

gggacaagaa gccgcccgcct gctgccccgg gcccggggag ggggctgggg ctggggccgg 180
aggcgggggtg tgagtgggtg tgtgcggggg gccgaggctt gatgcaatcc cgataagaaa 240
tgctcgggtg tcttggggcac ctaccctgtg ggcccgtgag gcgctactat ataaggctgc 300
cggccccggag ccgcccgcgc gtcagagcag gagcgtgcg tccaggatct agggccacga 360
ccatcccaac ccggcactca cagccccgca gcgcatcccg gtgcgcgcc agcctcccgc 420
acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgccgacgg 660
cgtcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720
tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgccga 780
cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgccctccgg tctccctgag 900
cagtgcctaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatcttct 960
gccccatgctg cccatggtcc cagaggagcc tgaggacctc agggggccact tgggaatctga 1020
catgttctct tcgcccctgg agaccgacag catggacca tttgggcttg tcaccggact 1080
ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccattgcccgg gcctcttcac 1140
tgcctgccagg ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260
tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320
tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380
gctgcactgt ctgagttctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440
aaaattctta tgtcaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacagtgat ccaactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa tccccctga 1740
ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800
ccatctccca gccaccagc cctctgcca cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttgctt aaaaatcagg aaaagaaaag 1920
atltgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacct 1980
gaaccctttc ccagcactt ggttttccaa catgatatt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgccccaaa ttatatttat gtatgtaagt 2100
gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1                      5                      10                      15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
                20                      25                      30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
    35                      40                      45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
    50                      55                      60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

&lt;210&gt; 60

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 60

atccgcccag atggctacaa tgtgta

26

&lt;210&gt; 61

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtccggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc cgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
 gctgctgctg cgctacctgg tggcgccct gggctatcat aaggcctatg ggttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggcctatt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtgggaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatata cggatcaaaa atgtgacaag aagtgatgcg gggaaatata gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540  
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600  
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720  
 atattcctgt gaagcccga attctgttgg atatcgagg tgcctggga aacgaatgca 780  
 agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840  
 ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900  
 ctccctccag aagagtaatt cttcatctaa agccacgaca atgagtgaat atgtgcagtg 960  
 gctcacgcct gtaatcccag cactttggaa ggccgcgcg ggcggatcac gaggtcagga 1020  
 gttctagacc agtctggcca atatggtgaa acccatctc tactaaaata caaaaattag 1080  
 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140  
 acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200  
 cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260  
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15  
 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                   35                                  40                                  45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
                   50                                  55                                  60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
                   65                                  70                                  75                                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                                   85                                  90                                  95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                                   100                                  105                                  110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                                   115                                  120                                  125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
                   130                                  135                                  140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
                   145                                  150                                  155                                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                                   165                                  170                                  175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                                   180                                  185                                  190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                                   195                                  200                                  205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
                   210                                  215                                  220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
                   225                                  230                                  235                                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                                   245                                  250                                  255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                                   260                                  265                                  270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                   275                                  280                                  285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
                   290                                  295                                  300  
 Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 65  
 atcgttgatga agttagtgcc cc 22

<210> 66  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 66  
 acctgagata tccaacagaa ttg 23

<210> 67  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 67  
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 68  
 gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60  
 agaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120  
 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
 aaataaatga attactcaat ctctatgac catctataca tactccacct tcaaaaagta 240  
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300  
 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtgggttcta 360  
 tggcattcat catttgacaa atgcaagcat cttccttatc aatcagctcc tattgaactt 420  
 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540

```

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
ttacacccag atccatttat atggaagcat ctacagtga ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaataactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcttttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatat atcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggt tgatgctctt ccaaactctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
tctcttttta cgataacagg cttattaaag taccatgtgt tgctcttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500
tgaacagcaa tgctctcagt gcctgtacc atgggtaccat tgagtctctg ccaaacctca 1560
aggaaatcag catcacagct aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620
tgaacaaaac caacattcga ttcattggagc cagattcact gttttgcgtg gaccacctg 1680
aattccaagg tcagaatggt cggcaagtgc atttcagga catgatggaa atttgtctcc 1740
ctcttatagc tcctgagagc tttccttcta atctaaatgt agaagctggg agctatgttt 1800
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860
gtcaaaaact cttgccta atccctgacag acaagttcta tgtccattct gagggaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtga tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaactca gtgttaaag gacagccttt gtcaagactg 2160
aaaattctca tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaaggttt gcaccctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tcttatcagc tgctctctc cagaaatgaa ctgtgatggg ggacacagct 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
  1                      5                      10                      15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
          20                      25                      30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
      35                      40                      45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
      50                      55                      60

```

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
 65 70 75 80  
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190  
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300  
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320  
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340					345					350					
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
		355					360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
		370					375					380			
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385							390					395			400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
			420					425					430		
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435					440					445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
		450					455					460			
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465							470					475			480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490					495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
			500					505					510		
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
		515					520					525			
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
		530					535					540			
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545							550					555			560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
			580					585					590		
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
		595					600					605			
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
		610					615					620			

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens

<400> 70  
gcccgggact ggcgcaaggt gccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60  
agctgcagcc ttttgaacaa cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120  
ttaccacgct tgttggagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180  
gaatctggta gacctgtggt taaccctgtt cctctccatg tgtctcctcc tacaagttt 240  
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300  
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360  
tcttctcct gaaacagtct tactgtatct ggactccaat cagatcacat ctattcccaa 420  
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480  
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540  
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600  
aattgccaac aacctctggc actgcgactg tactctacag caagtctga ggagcatggc 660  
gtccaatcat gagacagccc acaacgtgat ctgtaaaaacg tccgtgttgg atgaacatgc 720  
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780  
taccgattat gccatgctgg tcaccatggt tggctggttc actatggtga tctcatatgt 840  
ggtatattat gtgaggcaaa atcaggagga tgcccggaga cacctcgaat acttgaaatc 900  
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960  
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020  
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgat 1080  
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140  
cacccttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200  
tagatccatc tcaactatta ataatgaaat ttattttttt aatttaaaag caaataaaag 1260  
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15  
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30  
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80  
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140  
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160  
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175  
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190  
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205  
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220  
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240  
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255  
 Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

accgagccga gcggaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgccc agccccctcc tggcctgctg gcagcccata ctctgctgg 120
tgctgggctc agtgctgtca ggctcgccca cgggctgccc gcccgcctgc gactgctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gagggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag ctccccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tgagagcccg cgccctcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcgtt atcctactgg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttgccgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccata cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggtcccg gcacctcaac atcaatgcc 720
tccgggacta ctcttcaag aggtgtgacc gactcaaggc cttggagatc tcccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgccct acctggcgtc ccgccaccta gtctatctcc 900
gcttctcaa cctctctac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gcgggcagct ggccgtggtg gaggccatg 1020
ccttcgcggc cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tgaggaatc agtcttccac tcggtgggca acctggagac actcatcctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttcggcg ccgctggcg ctcaacttca 1200
accggcagca gccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgcc aactacttca cctgcgcgcg cggccgcata cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgaccgcgc gcccgccatc ctctggctct caccgcgaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gtcacagtc ttccctgatg gcacgctgga ggtgctgtac gccagggtac 1500
aggacaacgg caggtacctg tgcacgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccac aagaccttcg 1620
ctttcatctc caaccagccg ggcgaggag aggccaacag caccgcgcc actgtgcctt 1680
tccccttcga catcaagacc ctcatcatcg ccaccaccat gggcttccat tcttctctgg 1740
gctcgtcct ctctgctg gtgctgctgt ttctctggag ccggggcaag ggcaacaca 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgccc 1860
acgcgcccc caagttcaac atgaagatga tatgagccg gggcgggggg cagggacccc 1920
cgggcggccg ggcaggggaa ggggcctggt cgccacctgc tcaactctca gtccctccca 1980
cctcctccct acccttctac acacgttctc tttctccctc ccgcctccgt cccctgctgc 2040
ccccgcag ccctcaccac ctgcctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

```

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1           5           10          15

```

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30  
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45  
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110  
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125  
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140  
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160  
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175  
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

	580		585		590										
Ile	Glu	Ile	Glu	Tyr	Val	Pro	Arg	Lys	Ser	Asp	Ala	Gly	Ile	Ser	Ser
	595						600					605			
Ala	Asp	Ala	Pro	Arg	Lys	Phe	Asn	Met	Lys	Met	Ile				
	610						615				620				

&lt;210&gt; 74

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 74

tcacctggag cctttattgg cc

22

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 75

ataccagcta taaccaggct gcg

23

&lt;210&gt; 76

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg  
gg

50

52

&lt;210&gt; 77

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77  
 ccatgtgtct cctcctacaa ag 22

<210> 78  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
 gggaatagat gtgatctgat tgg 23

<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 79  
 cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg 50

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 80  
 agcaaccgcc tgaagctcat cc 22

<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 81  
 aaggcgcggt gaaagatgta gacg 24

<210> 82

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcgggtca 60  
 acatcgtagt ccacccccctc cccatcccca gcccccgggg attcaggctc gccagcgccc 120  
 agccaggagag cgggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180  
 tcctgctgtt cgcctgctgc tgggcgcccc ggggggccc aa cctctcccag gacgacagcc 240  
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtgggtgctc aagtgccaaag 300  
 tgaaagatca cgaggactca tccctgcaat ggtctaacc tgetcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgccaagt cctcgctcac tgtgctagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660  
 tccacggaga accaaccgac atacaggaag atcccaatgg taaaaccttc actgtcagca 720  
 gctcggtgac attccagggt acccgggagg atgatggggc gaggcatcgtg tgctctgtga 780  
 accatgaatc tctaaaggga gctgacagat ccacctctca acgattgaa gttttataca 840  
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgagggccag aagctgttgc 900  
 tacactgtga gggcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgcctgat ctccctttc ctcaacaaga 1020  
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080  
 acaccctcaa tgtaaatgac cccagtccgg tgccctctc ctccagcacc taccacgcca 1140  
 tcatcggtgg gatcgtggct ttcattgtct tctgctgct catcatgctc atcttccttg 1200  
 gccactactt gatccggcac aaaggaaact acctgacaca tgaggcaaaa ggctccgacg 1260  
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtca ggaggggacg 1320  
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc cagggggcct 1380  
 gtggggactg ctggggccgt caccaacccg gacttgtaca gagcaaccgc agggccgccc 1440  
 ctcccgttg ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggt 1500  
 tttgtactcg gtttggaatg gggaggagg agggcgggg gaggggaggg ttgccctcag 1560  
 ccctttccgt ggcttctctg catttggtt attattatt ttgtaacaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met 1	Gly	Ala	Pro	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Ala
5								10						15	
Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
20								25					30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
35							40					45			
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
50						55					60				
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
65					70					75					80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
85									90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
100								105					110		
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
115							120					125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
130						135					140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
145					150					155					160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
165									170					175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
180								185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
195							200					205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
210						215					220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
225					230					235					240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
245									250				255		
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
260								265					270		
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
275							280					285			

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 87

cctagcacag tgacgaggga cttggc

26

&lt;210&gt; 88

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtcagtott ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

gggggttagg gaggaaggaa tccaccccca ccccccaaaa cccttttctt ctccctttcct 60
ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatggtc 120
gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240
agagaagatc tgttcctgca atgagataga aggggacctc cacgtagact gtgaaaaaaaa 300
gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggg 420
tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccggggggctt ttctggggct 480
gcagctggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540
ttttctgggg ctggacgatc tggaatatct ccaggctgat ttttaatttat tacgagatat 600
agaccggggg gccttcaggg acttgaacaa gctggagggtg ctcattttaa atgacaatct 660
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tcgacctccg 720
gggtaacagg ctgaaaacgc tgccctatga ggaggtcttg gagcaaattc ctggtattgc 780
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840
atggctggaa aacattccca agaatgccct gatcggccga gtggtctgcg aagccccac 900
cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttggtgc ctttgaaaaa 960
ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagacctttg ctctggacc 1020
cctgccaaact ctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```

```

aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140
agcgacgggt agctccagga acaaaccctt agctaacagt ttaccctgcc ctgggggctg 1200
cagctgcgac cacatcccag ggctcgggttt aaagatgaac tgcaacaaca ggaacgtgag 1260
cagcttggct gatttgaagc ccaagctctc taacgtgcag gagcttttcc tacgagataa 1320
caagatccac agcatccgaa aatcgcactt tgtggattac aagaacctca ttctgttga 1380
tctgggcaac aataacatcg ctactgtaga gaacaacact ttcaagaacc ttttggacct 1440
caggtggcta tacatggata gcaattacct ggacacgctg tcccgggaga aattcgcggtg 1500
gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccggtg 1560
cactttcaat gccatgcccc aactgaggat cctcattctc aacaacaacc tgctgaggtc 1620
cctgcctgtg gacgtgttcg ctgggggtctc gctctctaaa ctcagcctgc acaacaatta 1680
cttcatgtac ctcccgggtg caggggtgct ggaccagtta acctccatca tccagataga 1740
cctccacgga aacccctggg agtgctcctg cacaattgtg cttttcaagc agtgggcaga 1800
acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgcggg tgaacttctt 1860
tagaaaggat ttcattgctc tctccaatga cgagatctgc cctcagctgt acgctaggat 1920
ctcgcccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga ccgggacgca 1980
ctccaactcc tacctagaca ccagcagggt gtccatctcg gtgttgggtc cgggactgct 2040
gctggtgttt gtcacctccg ccttcaccgt ggtgggcatg ctcgtgttta tcctgaggaa 2100
ccgaaagcgg tccaagagac gagatgccaa ctctcccgcg tccgagatta attccctaca 2160
gacagtctgt gactcttct actggcacia tgggccttac aacgcagatg gggcccacag 2220
agtgtatgac tgtggctctc actcgctctc agactaagac cccaacccca ataggggagg 2280
gcagagggaa ggcatatacat cttcccccac cgcaggcacc ccgggggctg gaggggctg 2340
tacccaaata ccgcgcgcat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tgagagagct ggagagcgca gccagctcgc tctttgctga gagcccttt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgcctcgc cctcgcccc ggggcctgtg 2580
gggttggatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatctattt ttcccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755

```

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

```

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                      15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
          20                      25                      30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
          35                      40                      45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
          50                      55                      60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
          65                      70                      75                      80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
          85                      90                      95

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

670

agtcgactgc	gtccctgtga	cccggcgcca	gctgtgttcc	tgaccccca	ataactcagg	60
gctgcaccgg	gcctggcagc	gctccgcaca	catttcctgt	cgcggcctaa	gggaaactgt	120
tggccgctgg	gcccgcgggg	ggattcttgg	cagttggggg	gtccgtcggg	agcgagggcg	180

```

gaggggaagg gaggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggc cggcgttcgc cctgtgcctc ctctggcagg cgctctggcc 360
cgggccggggc ggccggcgaac accccaactgc cgaccgtgct ggctgctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatcct 480
gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
cctgcgggca ggcccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
ggagcgcagg cgttcccact gcaccctgga gaacgagcct ttgcgggggt tctcctggct 660
gtcctccgac ccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
ctcctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggtcg agcccgagg 780
ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
ggtcttgtgt cctgcgccgc gccccggggc cgctctaac ttgagctatc gcgcgccctt 900
ccagctgcac agcgcgcgtc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
ccggggacag ctcccgatct cagttacttg catcgccgac gaaatcggcg ctgcgtggga 1020
caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaagt 1080
cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgcctcggg 1140
cttcgagctg gggaaaggag gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200
tggggggacc ggggtgccc caggcgccc ccggccact gcaaccagcc ccgtgccgca 1260
gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccacttg tccctgaaca 1320
agacaattca gtaacatcta ttctgagat tcctcgatgg ggatcacaga gcacgatgtc 1380
tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccatc cagggagcgt 1440
gatttccaag tttaattcta cgacttcctc tgccactcct caggctttcg actcctcctc 1500
tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg cttgtcaagc tctgctttca cgaaagcccc tcttcccagc caaggaagga 1620
gtctatgggc ccgcggggc tggagagtga tcctgagccc gctgctttgg gctccagttc 1680
tgcacattgc acaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
gggtgccttg ctggcggagt cccctcttgg ctctagtgat gcatagggaa acaggggaca 1800
tgggcactcc tgtgaacagt ttttactttt tgatgaaacg gggaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc cccttccct aaattccctt tactccactg 1920
aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtga tactggggga ccgggtagtg ctggggagag atattttctt atgtttatct 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctaccaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat 2226

```

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
  1                      5                      10                     15

```

```

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
                20                      25                     30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
    35                      40                     45

```

```

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
    50                      55                     60

```

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285  
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300  
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335  
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340					345					350					
Ser	Thr	Met	Ser	Thr	Leu	Gln	Met	Ser	Leu	Gln	Ala	Glu	Ser	Lys	Ala
		355					360					365			
Thr	Ile	Thr	Pro	Ser	Gly	Ser	Val	Ile	Ser	Lys	Phe	Asn	Ser	Thr	Thr
		370					375					380			
Ser	Ser	Ala	Thr	Pro	Gln	Ala	Phe	Asp	Ser	Ser	Ser	Ala	Val	Val	Phe
		385					390					395			400
Ile	Phe	Val	Ser	Thr	Ala	Val	Val	Val	Leu	Val	Ile	Leu	Thr	Met	Thr
				405					410					415	
Val	Leu	Gly	Leu	Val	Lys	Leu	Cys	Phe	His	Glu	Ser	Pro	Ser	Ser	Gln
				420					425					430	
Pro	Arg	Lys	Glu	Ser	Met	Gly	Pro	Pro	Gly	Leu	Glu	Ser	Asp	Pro	Glu
				435					440					445	
Pro	Ala	Ala	Leu	Gly	Ser	Ser	Ser	Ala	His	Cys	Thr	Asn	Asn	Gly	Val
				450					455					460	
Lys	Val	Gly	Asp	Cys	Asp	Leu	Arg	Asp	Arg	Ala	Glu	Gly	Ala	Leu	Leu
				465					470					475	480
Ala	Glu	Ser	Pro	Leu	Gly	Ser	Ser	Asp	Ala						
				485					490						

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 99  
 acagagcaga gggtgccttg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 100  
 tcagggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 101  
 tcagggaagg agtgtgcagt tctg 24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgcctcgt 50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatccccggg ctacctgggc cgccccggcg cgggtgcgcgc gtgagagggg gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtctgt gccagtgtga gcggcggtgt gagcgcggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg cgccgtgggg tgcaaaccac gagcgtctac 300
gctgccatga ggggcgcgaa cgccctgggc ccactctgcc tgcctgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gattttattgg cagtgaagggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaaggga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaca cagctggcaa tggcttcatg 720
gccatgttct ccgctgtctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
gacagacctt ccggtctctt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttggt tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtc accctgcgca 1020
attgtgtctg agagaaatg acttcttatt cagtttttat cagacttaag ttttaactgca 1080
gatgggttta ttggctacta catattcagg ccaaaaaaac tgctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggtttaaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tcgtctgcaa gcagtgcctt ctctcagaa gaggtctaaa ttacattatt 1440
atgggccaag taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca tttaagctgt attctgccat tgcccttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttgga gcgtttatct atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1                      5                      10                      15

```

```

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                20                      25                      30

```

```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
        35                      40                      45

```

```

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
        50                      55                      60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360				365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390					395					400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
				405					410					415	

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcgagcgcg tgggcggccc acggcgcccg cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctcccag tcttctcccc cgcctcagcc ccattcgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagaac catccgggac 300
aactttggag gtggaaacac tgctgggag gaagagaatt tgtccaaata caaagacagt 360
gagaccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgcctgctgg agctgagtga ggagctggtg gagagctggt ggtttcacaa gcagcaggag 480
gccccggacc tcttcagtg gctgtgctca gattccctga agctctgctg ccccgaggc 540
accttcgggc ctcctgcct tcctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactgtt tgcaatgcaa gaaggctgg gccctgcac acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgctg gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaa gctgcctag gctgcatggg ggcagggcca 960
ggtcgctgta agaagtgtag ccctggctat cagcagggtg gctccaagtg tctcgatgtg 1020
gatgagtgtg agacagaggt gtgtccggga gagaacaagc agtgtgaaaa caccgagggc 1080
ggttatcgct gcatctgtgc cgagggtac aagcagatgg aaggcatctg tgtgaaggag 1140
cagatcccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcgcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggttc atcaaggcca gataatcgcg gccaccacct 1380
gtaggacctc ctcccaccca cgctgcccc agagcttggg ctgcccctct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gcccaggtag ccaggcccg gacagacaagg cccctggggt aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttctt taatggtggc tgctagagct ttggccctg cttaggatta ggtggtcctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tctgttctg 1740
tgttcaccac atccccacac ccatttgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgga agttaaaaa aaaaaaaaa aaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1                      5                      10                      15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20                      25                      30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35                      40                      45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50                      55                      60

```

Arg	Asp	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu	65	70	75	80
Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly	85	90	95	
Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser	100	105	110	
Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro	115	120	125	
Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro	130	135	140	
Ala	Gly	Thr	Phe	Gly	Pro	Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu	145	150	155	160
Arg	Pro	Cys	Gly	Gly	Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly	165	170	175	
Gly	Ser	Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Gly	Glu	Ala	Cys	180	185	190	
Gly	Gln	Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ala	Ser	His	195	200	205	
Leu	Val	Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Ser	Gly	Pro	210	215	220	
Glu	Glu	Ser	Asn	Cys	Leu	Gln	Cys	Lys	Lys	Gly	Trp	Ala	Leu	His	His	225	230	235	240
Leu	Lys	Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gly	Ala	Asn	Cys	245	250	255	
Gly	Ala	Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg	260	265	270	
Asp	Cys	Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Arg	275	280	285	
Cys	Lys	Lys	Cys	Ser	Pro	Gly	Tyr	Gln	Gln	Val	Gly	Ser	Lys	Cys	Leu	290	295	300	
Asp	Val	Asp	Glu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Gly	Glu	Asn	Lys	Gln	305	310	315	320
Cys	Glu	Asn	Thr	Glu	Gly	Gly	Tyr	Arg	Cys	Ile	Cys	Ala	Glu	Gly	Tyr	325	330	335	
Lys	Gln	Met	Glu	Gly	Ile	Cys	Val	Lys	Glu	Gln	Ile	Pro	Glu	Ser	Ala	340	345	350	

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
       370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tcctccaggg 60  
 cagcaccatg cagcccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120  
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcacccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctggtgttc ggcatggagc agcggctgcc gcccaacagc gagctggtgc aggcctgct 420  
 gcggctcttc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480  
 gcgcagcgcc cggggccggg tgaccgtcga gtggtgcgc gtccgcgacg acggctccaa 540  
 ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agcgcgtgct 660  
 gctacaggtg tcggtgcaga gggagcatct gggcccgtg gcgtccggcg cccacaagct 720  
 ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtggc 900  
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960  
 gcagcccccg gaggcctggt ccttcaagtg gccgtttctg gggcctcgac agtgcctgc 1020  
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080  
 ccagggtggtc agcctgcccc acatgagggg gcagaagtgc agctgtgctt cggatggtgc 1140  
 gctcgtgcca aggaggtcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgctct ctagtgagcc ctgaatttgc ttctctgac aagttacctc 1320  
 acctaatatt tgcttctcag gaatgagaat tcttggccac tggagagccc ttgctcagtt 1380  
 ttctctatct ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440  
 aactgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500  
 aaagtccctc accaccactc tggacctaaag acctgggggt aagtgtgggt tgtgcacccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                  345                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
           355                  360                  365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 115

aggactgccca taacttgcct g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcttgatcgc gatggggaca 60  
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgtctcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgat cctacgaatc ccaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tcccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780
ctgtaaacc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtgcgccga gtgaaggaga attcaaacag acctcgatc tctgggtgtg agcctggctg 960
gctcaccgcc tatcatctgc atttgcctta ctcaggtgct accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tcttctatgc cctccctccc 1140
tttctacca ctgctgagtg gcctggaact tgttttaaagt gtttattccc catttctttg 1200
agggatcagg aaggaatcct gggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tggcgggggg cgcaggaatc tgcactcaac tgcccaactg gctggcaggg atctttgaat 1320
aggtatcttg agcttgggtc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttgggtgat gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaacc tactggaaat acaaagttag ccaggcatgg tggatcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
                   100                  105                  110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
                   115                  120                  125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
                   130                  135                  140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145                  150                  155                  160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
                   165                  170                  175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
                   180                  185                  190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
                   195                  200                  205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
                   210                  215                  220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225                  230                  235                  240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
                   245                  250                  255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
                   260                  265                  270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
                   275                  280                  285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
                   290                  295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctggt tccc

24

<210> 121

<211> 50

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50  
  
 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctgggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

```

cagcgcgtgg ccggcgccgc tgtgggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctgggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagcc atgtaccag aaagggaat gccaccgcc cctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt cactcacgt 480
ggcgctgcca cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc cctgtgacc ctggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggg caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgctcct gccactggg gttactggg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcy tagccggaca ggaggagagc agtgatgcgg atgggtacct 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
tcctgcagaa gtggccctgg agattgaggg tcctgggaca ctccctatgg agatccgggg 1080
agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc
1210

```

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1             5             10             15

```

```

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
      20             25             30

```

```

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
      35             40             45

```

```

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
      50             55             60

```

```

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
      65             70             75             80

```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                             85                            90                            95  
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                             100                            105                            110  
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                             115                            120                            125  
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                             130                            135                            140  
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                             145                            150                            155                            160  
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                             165                            170                            175  
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                             180                            185                            190  
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                             195                            200                            205  
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                             210                            215                            220  
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                             225                            230                            235                            240  
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                             245                            250                            255  
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                             260                            265                            270  
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                             275                            280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgtc cggctctcgt cgctcgcgca gcggcggcag cagaggctgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatgggttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagaag 420
gattcaagct gaaggcgctt acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatac 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600
atgaaggatt caagatccgg taccgagacc tacacaatat ggtttcatta tgcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctoct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggg gagtcacgga gatttcgtct gccaccgcgc gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgata ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtgggttc cttcttatca agtctactgc atcaaatac 1080
agcaaacgtg gccagacacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140

```

```

cggcaaccag tgtgctgctg gtgctgctgc tegtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctcgccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccg 1380
tggaagacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcataccatca tgcccactgg gtgttggtcc 1620
taagaaactg attgattaaa aaattttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1             5             10             15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
      35             40             45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
      50             55             60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
      65             70             75             80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
      100            105            110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
      115            120            125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
      130            135            140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
      145            150            155            160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165            170            175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

180					185					190					
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200						205		
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
	210					215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230					235					240
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245					250					255	
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
			260					265					270		
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
		275					280					285			
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
	290					295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					320
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
			325						330					335	
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
			340					345					350		
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
		355					360					365			
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
	370					375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					400
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
				405					410					415	
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
			420					425					430		
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
		435					440					445			
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
	450					455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
 atctcctatc gctgctttcc cgg 23

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc 23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaciaa aaccttatct 50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgctg cggtcogtgc gtggcctaga 60  
 gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg ccgcccagcc cgctccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttgac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

```

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgctgca 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctctctctcc 900
ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgaggagcagc 960
cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagacc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgta ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaagtg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgttggg acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga cttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tgggttggtt tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<210> 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaagggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgagg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240  
 cctgcaccag cggcggggtgg ccttggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctgggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaaccca caggaggtct ttattcgttc 660  
 cactaacatt tttcgggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720

```

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
cacatccttg tacatactgc ccaaggaaga cagggaaagt cttcagatgg cagtaggccc 1080
attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgcccccca 1140
caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
gaccctgggg atttttgacc acaaattggc accggttgct gttgacctga ccatggaact 1260
ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agttttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

```

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
  1             5             10             15

```

```

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

```

```

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

```

```

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

```

```

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

```

```

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

```

```

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

```

```

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

```

```

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

```

```

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

```

```

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

```

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa cataacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccacaga 480
gagctctttc tccccagtc cagaggggtg caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggctg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cctttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgtat ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtgta tgcaagcaac tgggctgtgg 960
gaagtccctc tctccctcct tcagagaccg gaaatgctat ggccctgggg ttggccgcat 1020
ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080
attttggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgtg 1140
ggtgggcatc atctaactctg ttgagtgcct gaatagaaga aaaacacaga agaaggagc 1200
atttactgtc tacatgactg catgggatga aactgatct tttctgccc ttggactggg 1260
acttatactt ggtgcccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320
aggtctagtt ctcaggccat cagacatagt ttggaactac atcaccacct ttcctatgtc 1380
tcacattgc acacagcaga tcccagcct ccataattgt gtgtatcaac tacttaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt gggttatggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

```

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

```

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115                      120                      125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130                      135                      140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145                      150                      155                      160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
165                      170                      175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180                      185                      190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195                      200                      205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210                      215                      220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225                      230                      235                      240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245                      250                      255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260                      265                      270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275                      280                      285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
290                      295                      300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
305                      310                      315                      320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
325                      330                      335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
340                      345

```

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

```

actgcaactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcacctcg 60
acccacgcgt ccgcggacgc gtgggcggac gcgtgggccc gctaccagga agagtctgcc 120
gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcgggctg 180
cctgggcgctc ttccggcctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240
gaatgctgtg gtgggtgatca caggcgccac ctgagggtg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
gtgcttttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat tccttttcga tcagcatatg cagcctccaa 720
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaatg ccatcaccgc 840
ggatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gccctgtgga 900
ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
cttactgcct tccttggctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```

```

agggccaggg cagagaagca gcaactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc cagggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttgcccgcc atggccaac ttgtttattg cagcttataa tggttac 1427

```

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1             5             10             15

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20             25             30

```

```

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35             40             45

```

```

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50             55             60

```

```

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65             70             75             80

```

```

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85             90             95

```

```

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100            105            110

```

```

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115            120            125

```

```

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130            135            140

```

```

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145            150            155            160

```

```

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165            170            175

```

```

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180            185            190

```

```

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195            200            205

```

```

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

```

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

ggtgctaaac tggctgctctg tggc

24

&lt;210&gt; 155

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

cagggcaaga tgagcattcc

20

&lt;210&gt; 156

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156  
tcatactggtt ccatctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattggggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360  
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtgtag tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaacaa catgtctgtg tcctaatttc gtaaacactg gttcatcaa 780  
aaatccaagt acaagtttgg gacccactct ggaacctgag gaagtggtaa acaggctgat 840  
gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtg 960  
taagtttgat gcagttattg gatataaaat gaaagcgcaa taagcaccta gttttctgaa 1020  
aactgattta ccaggtttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080  
cttctgtttt ttctaattat cccatttct tcaatatcat ttttgaggct ttggcagtc 1140  
tcatttacta ccactgttct tttagccaaa agctgattac atatgatata aacagagaaa 1200  
tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac tttattaaaa 1260  
taatttccaa gattatttgt ggctcacctg aaggctttgc aaaatttgta ccataaccgt 1320  
ttatttaaca tatattttta tttttgattg cacttaaat ttgtataatt tgtgtttctt 1380  
tttctgttct acataaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440  
tagtggatatt tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctaccatt 1500  
gccactctgt ttctgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560  
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620  
agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1771

<210> 159

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val  
 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
 20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
 50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
 100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr  
 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
 245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg 23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc 24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

```

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct caccctttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc ttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacia cagcaacctc 360
ttcttctggt tcttcccagc tcagatacag ccagaagatg ccccagtagt tctctggcta 420
caggggtgggc cgggagggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatttctctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcttttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat ttttgtcact cccagagggtg agacaagcca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200
ccatgggttaa ctgaaatcat gaataattat aagggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgccct gacagagcgc tcttgatgg gcattggactg gaaaggatcc 1320
caggaatata agaaggcaga aaaaaaagtt tggaagatct ttaaactctga cagtgaagtg 1380
gctgggttaca tccggcaagc ggggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttagggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaag agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1             5             10             15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20             25             30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35             40             45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50             55             60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65					70					75					80
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225				230						235				240	
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305				310						315				320	
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctggcatc aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggcctt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggtacaaac 60  
 atttttccct ttctaataaa gttctaacag ctgttctaac agctagtcat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tccttgcttc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240  
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctgggggagg gctgccttaa caagctttca aaaaacagga gcgacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat aggggaagact ggggttagtc ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600  
 gagaaagtat gttaaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
 accaggatgg ggaccctggg tcaggccagc ctctttgtct ctcccggaaa ttatttttgg 720  
 tctgaccact ctgccttgtg ttttgcagaa tcatgtgagg gccaaaccgg gaaggtggag 780  
 cagatgagca cacacaggag ccgtctcctc accgccgccc ctctcagcat ggaacagagg 840  
 cagccctggc cccgggccct ggaggtggac agccgctctg tggtcctgct ctcagtggtc 900  
 tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960  
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
 ggggccatca accgggtcta taagctgaca ggcaacctga ccatccagggt gggtcataag 1080  
 acagggccag aagaggacaa caagtctcgt taccgcgccc tcatcgtgca gccctgcagc 1140  
 gaagtgtcga ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200  
 cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgctgag gctggatgac 1260  
 ctcttcaccc tgggtggagc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320  
 acgggcacca tgtacggggg gattgtgcgc tctgaggggt aggatggcaa gctcttcac 1380  
 ggacaggctg tggatgggaa gcaggattac ttcccgaccc tgtccagccg gaagctgccc 1440  
 cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500  
 ctcatcaaga tcccttcaga caccctggcc ctggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagccgga gaccctgag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct cagcatcgt gcggctctgc 1680

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct tcggctgcac ccggggccggg 1740
gtggaataacc gcctcctgca ggctgcttac ctggccaagc ctgggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccgga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980
tggctgctgg ggaaggacgt ccagtgcacg aaggcgctg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggctacagc 2160
gtgggtttttg tggggactaa gagtggcaag ctgaaaaagg taagagtcta tgagttcaga 2220
tgctccaatg ccattcacct cctcagcaaa gagtccctct tggaaggtag ctattggtgg 2280
agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaaga 2340
aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400
gtaaggaatg caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100              105              110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115              120              125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130              135              140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145              150              155              160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165              170              175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190  
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205  
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220  
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240  
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255  
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270  
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285  
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300  
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320  
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335  
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350  
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365  
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380  
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400  
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415  
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445  
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450	455	460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr		
465	470	475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly		
	485	490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val		
	500	505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys		
	515	520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln		
	530	535 540
Leu Tyr Phe Leu Gly Glu Gln Arg		
545	550	

&lt;210&gt; 171

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 171

tggaataaccg cctcctgcag

20

&lt;210&gt; 172

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 172

cttctgccct ttggagaaga tggc

24

&lt;210&gt; 173

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
aggctccccg gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60  
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcgt cttgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggtccttc 180  
tgcggtcccg ccatcgacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240  
attccacctt ctggatcttc gggggctcca tccactatct ccgtgtgccc agggagtact 300  
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360  
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420  
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggccct 480  
acatctgcag tgagatggac ctcggggctg tgcccagctg gctactccaa gacctggca 540  
tgaggctgag gacaacttac aagggttca ccgaagcagt ggacctttat tttgaccacc 600  
tgatgtccag ggtggtgcc ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660  
tgagaaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720  
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780  
gcaaggggat tgtccagga gtcttgacca ccatcaactt gcagtcaaca cagagctgc 840  
agctactgac cactttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900  
acttgacggg gtggtttgac tcgtggggag gccctcaca tatcttgat tctctgagg 960  
ttttgaaaac cgtgtctgcc attgtggacg ccggtcctc catcaacctc tacatgttcc 1020  
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtcag 1080  
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140  
acatgaagct tcgagacttc ttcggtcca tctcaggcat cctctcctc ccccccactg 1200  
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260  
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320  
tgccagtcaa tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380  
cctcgtctgg catcctcagt ggccacgtgc atgatcggg gcagggtgtt gtgaacacag 1440  
tatccatagg attcttgac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500  
acaccgtgct gaggatcttg gtggagaatc gtgggcgagt caactatggg gagaatattg 1560  
atgaccageg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620  
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680  
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740  
gctccacgcc ttgtgacacc tttctgaagc tgagggctg ggagaagggg gttgtattca 1800  
tcaatggcca gaaccttga cgttactgga acattggacc ccagaagacg ccttacctcc 1860  
caggtccctt gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920  
gccctgcatt acagttcacg gaaaccccc accctgggcag gaaccagtac attaagttag 1980  
cggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2040  
ctgggtggct ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100  
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160  
ggatggctct gggcctggct ttgttgatga tggttttct acagccctgc tctgtgccc 2220  
aggctgtcgg gctgtctcta ggggtgggag agctaatac atcgcccagc ctttggccct 2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
gactcaggcg tgctctttgc tggttcctgg gaggcttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttccccctt tcccttccca ctgctgctt cccacagggt 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtg 2640
ctctggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1                      5                      10                      15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
                20                      25                      30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
                35                      40                      45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
  50                      55                      60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
  65                      70                      75                      80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
                85                      90                      95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
                100                      105                      110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
  115                      120                      125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
  130                      135                      140

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60  
ccctggtgag ggttctctac ttggccttcg gtgggggtca agacgcaggc acctacgccca 120  
aaggggagca aagccgggct cggcccaggg cccccaggac ctccatctcc caatgttggg 180  
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgccca 240  
tggtcctccaa gaagctgtcc tgcttcgtt cctgtctgct gccgtcagc ctgacgctac 300  
tgctgccccca ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360  
tagacggggc cccgttcgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

```

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cttcgaaaac 660
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctggttca 720
aggtccttgc gcccaagata tatccatggc tttatcacaa tgggggcaac atcattagca 780
ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080
ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtgccat aagaaggagc 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatactctgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttcctttgg 1320
gacctttacc tcccccgagc cccaagatga tgccttggacc tgtgactctg caoctgggtg 1380
ggcctttact ggctttccta gacttgcttt gcccccggtg gcccatctcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
cccataccat ttttgagcca accacttct ggggtccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg gggccaaaac tggatatctt ggtggagaac atggggaggc 1680
tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggtttcccct ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggtctag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980
ggccacaaca gacctctac gtgccaatgt tcctgctgtt tcctagggga gccctcaaca 2040
aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaac ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttggggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggaggttgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaaa 2505

```

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

```

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20              25              30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35              40              45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50              55              60

```

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80  
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95  
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110  
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125  
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140  
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160  
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175  
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190  
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205  
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220  
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro  
 225 230 235 240  
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255  
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270  
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285  
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300  
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320  
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335  
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340					345					350					
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro
		355					360					365			
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu
	370					375					380				
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu
385					390					395					400
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr
				405					410					415	
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val
			420					425					430		
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val
	435						440					445			
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr
	450					455					460				
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg
465					470					475					480
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro
				485					490					495	
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu
			500					505					510		
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys
		515					520					525			
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr
	530					535					540				
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly
545					550					555					560
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr
				565					570					575	
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu
			580					585					590		
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu
		595					600					605			
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu
	610					615					620				

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
645 650

```
<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 178  
tggctactcc aagaccctgg catg 24

```
<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179  
tggacaaatc cccttgctca gccc 24

```
<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

<400> 180  
gggcttcacc gaagcagtgg acctttat ttgaccacctg atgtccaggg 50

```
<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

```
<400> 181
ccagctatga ctatgatgca cc 22
```

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc 24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 gctttgaaca cgtctgcaag cccaaagtgt agcatctgat tggttatgag gtatttgagt 60  
 gcaccacaaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120  
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggttag accagtatga ccagctatat tccaagcggt 300  
 ttgggtgtgt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca ttccacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaactgg atttaaatgc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaaag tggacattct gccaaaacaa ttgtttaaat 1320

```

gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttgttgtg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggttttaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800
aggggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
gctgccgcta ctgaatgttt acaaattgct tgcttgctaa agtaaattgat taaattgaca 1920
ttttcttact aaaaaaaaaa aaaaaaaa 1947

```

&lt;210&gt; 185

&lt;211&gt; 501

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

```

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85             90             95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100            105            110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115            120            125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130            135            140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145            150            155            160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165            170            175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180            185            190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

```
<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence
```

<400> 186  
cctccctcta ttacccatgt c 21

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

<400> 187  
gaccaacttt ctctgggagt gagg 24

```
<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

<400> 188  
gtcacttttat ttctctaaca acaagctcga atccttacca gtggcag 47

```
<210> 189
<211> 2917
<212> DNA
<213> Homo sapiens
```

```
<400> 189
cccacgcgctc  cggcctttctc  tctggactttt  gcattttccat  tcttttttcat  tgacaaaactg  60
actttttttta  ttttctttttt  tccatctcttg  ggccagctttg  ggatcctagg  ccgcctctggg  120
aagacatttg  tgttttacac  acataaggat  ctgtgttttg  ggtttcttct  tctctccctg  180
```

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240  
 gcaatttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300  
 atcgttggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcctttac 360  
 ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420  
 cacaacccag acaaggtgtg gtggggccaag aacagccagg ccaaaacccat tgccacggag 480  
 tcttgctctg cctgacagt ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540  
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaaa 600  
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660  
 agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720  
 cagctgctgg agatccctac agagagcttc cactgggggc aacccttcca ggaaggagtt 780  
 ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840  
 ctcacacaaa tctacctctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
 gctgatgtaa cacagagcct ataaaagctg tcggctctta aggetgcccgc gcgccttgcc 960  
 aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020  
 gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080  
 aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140  
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tcttttctta tgtccagctt 1200  
 gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260  
 gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320  
 tccagtacat tgacgtttca aatagttact gactcagcaa gaattcaaag aactgtcttt 1380  
 gtcttctact acttcttctc tctaaccatc tctattccaa actgtggcgg ttacctggat 1440  
 accttggaag gatccttcac cagccccaat taccaaaagc cgcctcctga gctggcttat 1500  
 tgtgtgtggc acatacaagt ggagaaagat tacaagataa aactaaactt caaagagatt 1560  
 ttcctagaaa tagacaaaac gtgcaaat tt gattttcttg ccatctatga tggccctctc 1620  
 accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccacctt cgaatcgtca 1680  
 tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740  
 gcttcttaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800  
 gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860  
 aacttgcaac taaaagacct aacttgcaag ccaaaattat caaatgtgtt ggaattttct 1920  
 gtcctcttca atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980  
 aatataatca ctttttctgc atcctcaact tctgaagtga tcaaccgtca gaaacaactc 2040  
 cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100  
 gaagatgatg taatacaaa gtcaaaatgca ctgggcaaat ataacaccag catggctctt 2160  
 tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220  
 caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280  
 gatacctgta gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacaag 2340  
 agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400  
 ttcagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460  
 gttttgatat gtgatagcag tgaccaccag tctcgctgca atcaaggttg tgtctccaga 2520  
 agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580  
 ctgaaaaggg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgaggaa 2640  
 gaaactccaa accagccttt caacagtgtg catctgtttt cttcatggg tctagctctg 2700  
 aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760  
 aaataaccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820  
 tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880  
 ggctgaaaag tgacacacag gcctgcatgt aaaaaaa 2917

&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
 1 5 10 15  
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
 20 25 30  
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
 35 40 45  
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
 50 55 60  
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
 65 70 75 80  
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
 85 90 95  
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
 100 105 110  
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
 115 120 125  
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
 130 135 140  
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr  
 145 150 155 160  
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu  
 165 170 175  
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile  
 180 185 190  
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys  
 195 200 205  
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu  
 210 215 220  
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser  
 225 230 235 240  
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg  
 245 250 255  
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr  
 260 265 270  
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys  
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300  
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350  
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365  
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430  
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445  
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565		570		575										
Leu	Ala	Leu	Asn	Val	Val	Thr	Val	Ala	Thr	Ile	Thr	Val	Arg	His	Phe
			580					585					590		
Val	Asn	Gln	Arg	Ala	Asp	Tyr	Lys	Tyr	Gln	Lys	Leu	Gln	Asn	Tyr	
			595				600					605			

<210> 191  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
 tctctattcc aaactgtggc g 21

<210> 192  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
 tttgatgacg attcgaaggt gg 22

<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 gacggaagaa cagcgctccc gagggccgagg gagcctgcag agaggacagc cggcctgcgc 60  
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cgttgctgct gttgctgttg 120  
 ctgctgctgc cgccgcccgc gtgcctgcc cacagcgcca cgcgcttcca cccacactgg 180

gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaaagt cgccatcttc 240  
 atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtattgg 300  
 caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattacc tcctagtctc 360  
 aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgcaa ccagtgggca 420  
 gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480  
 tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540  
 agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgacct gcgttttggg 600  
 ctgtactatt ccttttttga atggtttcat ccgctcttcc ttgaggatga atccagtcca 660  
 ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720  
 aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780  
 aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtatgc 840  
 accaatgatc gttggggagc tggtagcatc tgaagcatg gtggcttcta tacctgcagt 900  
 gatcggtata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960  
 aaactgtcct ggggctatag gagggaaagt ggaatctctg actatcttac aattgaagaa 1020  
 ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattggg 1080  
 cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140  
 tggctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200  
 actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260  
 tttcttaaat ggccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320  
 gcaacagagg tgaaactact gggccatgga cagccactta actggatttc tttggagcaa 1380  
 aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440  
 tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500  
 atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560  
 aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620  
 ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680  
 cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740  
 gaattggtgg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800  
 tatatagtta tgcatactt aatatgggga tattttctgg gaaatgcatt gctagtcaat 1860  
 tttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920  
 cacaccta atgtgtatggt tagactgttg ctcttaggct acagacatat acagcatgtt 1980  
 actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040  
 gagaaggtag agtaaaaata ctgtaaaata aatgggtgcac ctgtataggg cacttaccac 2100  
 gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160  
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220  
 ttataaaaaa agttttttct ttcttcaatt ataaattaac ataagtgtac tgaacttta 2280  
 caaacgtttt aattttttaa acctttttgg ctcttttgta ataacactta gcttaaaaca 2340  
 taaactcatt gtgcaaatgt aa 2362

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu  
 1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr  
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
 35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
                   340                  345                  350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                  360                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                  375                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                  390                  395                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                   405                  410                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                  425                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                  440                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
                   450                  455                  460

Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198  
 aacttcgagc atcagccact ctgc 24

<210> 199  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199  
 ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca 45

<210> 200  
 <211> 2372  
 <212> DNA  
 <213> Homo sapiens

<400> 200  
 agcagggaaa tccgatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60  
 gttccagaac tctccatccg gactagtatt tgagcatctg cctctcatat caccagtggc 120  
 catctgaggt gtttccctgg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180  
 gtgttgcttc tcacttccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240  
 gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300  
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360  
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420  
 ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccaaaccc caagtgtggg 480  
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540  
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600  
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660  
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720  
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780  
 gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840  
 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900  
 tttggtgctc cagctgggtc tggattttgc tatgtcaaaa ggtatgtgaa ggcttccct 960  
 tttcaaaaca agaactagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020  
 gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaaccc agaagagtcc 1080  
 aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140  
 tgaggagaca cacctgaggc tggtttcttt catgctcctt accctgcccc agctggggaa 1200  
 atcaaaaggg ccaagaagacc aaagaagaaa gtccaccctt gggttcctaac tggaaatcagc 1260  
 tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320  
 cctgtctgga tctatctctc ctacctccaa agcttccac gccctttcta gcctggctat 1380  
 gtccctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```

tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggtg ggttgaaagc 1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagtttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgttttag aacacacaca cttacttttt ctggtctcta cactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct ggaagctat 2100
ttttttcagt ttgatattt ctagcttatt tacttccaaa ctaattttta tttttgtga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

```

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
  1              5              10              15

```

```

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20              25              30

```

```

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35              40              45

```

```

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50              55              60

```

```

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65              70              75              80

```

```

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85              90              95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100              105              110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115              120              125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130              135              140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggt aacctgtgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgagca catcaccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgcggcggcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gagcagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctt cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcacc ctaggaagg cctgccatgc 1080
tgtggccaac tgtttcactg gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctcaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatccct ggactttcac taacctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20

25

30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35

40

45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50

55

60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65

70

75

80

```
<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 208
gcttggatat tcgcatgggc ctac
```

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccga gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcttgcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgccc gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgcacctg cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctgggtg ccacgcgggt 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtggt 600

```

ctttccttac cagtccccca acggggegta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tggtagcctc ctttgagcag ctcttcggg cctgggagga 720
gggctggac tggtagaacg cgggctggct gcaggatgct acgggtgcagt accccatcat 780
gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840
ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgccc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgctacc ctgtggttca 1080
cccgcacct aactgtgggc cccagagacc tggggctcga agctttggct tccccgacct 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggccctcccc 1200
tgccgcattc cctcaactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad ttttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380
aatcatgctt gctccccctg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggctg gtctccctcc cttaaggagg ttggtgccc gagtgggagg tggcctgtct 1500
agaatgccgc cgggagtcgc ggcattgggt gcacagttct ccctgcccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
cttctctgtg aagccgctga cccagctctg cccactgagg ggctagggtt ggaagccagt 1680
tctaggcttc caggcgaaat ctgagggaag gaagaaactc cctccccgt tccccctccc 1740
ctctcggttc caaagaatct gttttgttgt catttgtttc tctgtttcc ctgtgtgggg 1800
aggggcccctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccaa 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa                                           1985

```

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

115					120					125						
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	
130					135					140						
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu	
145					150					155					160	
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg	
165					170					175						
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	
180					185					190						
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	
195					200					205						
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr	
210					215					220						
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro	
225					230					235					240	
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	
245					250					255						
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu	
260					265					270						
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu	
275					280					285						
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys	
290					295					300						
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	
305					310					315					320	
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu	
325					330					335						
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr	
340					345					350						
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His									
355					360											

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttggtg gggtggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ggagagcggg gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60  
 gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggcgagctt cgcgctgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcgcttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
 agccttcctg caccocgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660  
 ggaggacctg gacagaaaca aagatggcta tgtccaggtg gaggagtaca tcgcgatct 720  
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
 ggtgctgccc cctgccagg accagccctt ggtggaagcc aaccacctgc tgcacgagag 900  
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
 tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020  
 agcaccgcgc acctgccaca gctcagagg ccgcacaaat gaccggagga gggcgcgctg 1080  
 tggctctggc ccctccctgt ccaggcccc caggaggcag atgcagtccc aggcattctc 1140  
 ctgcccctgg gctctcagg accccctggg tcggcttctg tccctgtcac accccaacc 1200  
 ccaggggagg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260  
 cagcccagac ccagggaccc ttggcccca gctcagctct aagaaccgcc ccaaccctc 1320  
 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
 tgcttgccct ggccctgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440  
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75 80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155 160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235 240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 225

ccccctgag cgacgctccc ccatgatgac gccacggga actt

44

&lt;210&gt; 226

&lt;211&gt; 2403

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 226

```

ggggccttgc cttccgcact cggg'gcgcagc cgggtggatc tcgagcaggt gcgagagcccc 60
gggcggcgagg cgcggggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
ccagcctgtc tgtcgctggt ttggcgcccc cgccctcccc cggtgcgggg ttgcacaccg 180
atcctgggct togtcgatt tgccgcccag gcgcctcccc gacctagagg ggcgctggcc 240
tgagagcagc ggtcgtctgt gtctctctc ctctgcgcgc cgcccgggga tccgaagggt 300
gcggggctct gaggaggtga cgcgcggggc ctccgcacc ctggccttgc ccgcattctc 360
cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggtc 420
tcggcctcgg tgtgtgtctg ctgctgctgc cggggcccg gcgcagcag ggagccgtc 480
ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540
tctgcccagg gggtgcctt cttgaggaat tctctgtgta tgggaacata gtatatgtt 600
ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660
ctgtacgagt ctatagccta cctggctcag aaaactattc ctcagtagat gccaatggca 720
tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780
gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840
taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900
tgattgatgg aagctttaat attgggcagc gccgatttaa ttacagaag aattttgttg 960
gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020
ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
tgtttgccat aaaggaagta ggtttcagag ggggtaattc caatacagga aaagccttga 1140
agcatactgc tcagaaattc ttcacggtag atgctggagt aagaaaaggg atcccaaaag 1200
tggtgggtgg atttattgat gggtggcctt ctgatgacat cgaggaagca ggcattgttg 1260
ccagagaggt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320
tggggatggg tcaggatgtc acatttggtg acaaggctgt ctgtcggaat aatggcttct 1380
tctcttacca catgcccac tggtttggca ccacaaaata cgtaaagcct ctggtacaga 1440
agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500
cctttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560
ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620
tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680
atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggacagct actggtgatg 1740
ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860
cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920
tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gagttcacag 1980
gattagaacc aattgtttct gatgtcatc gaggcatttg tagagatttc ttagaatccc 2040
agcaataatg gtaacatttt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100
attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2160
gtatgtcaac agccatttag gcaataaagc actcctttaa agccgctgcc ttctggttac 2220
aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340
tgtacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400
aaa
2403

```

&lt;210&gt; 227

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

```

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
  1             5             10             15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
          20             25             30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
          35             40             45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
          50             55             60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
          65             70             75             80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
          85             90             95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
          100            105            110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
          115            120            125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
          130            135            140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
          145            150            155            160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
          165            170            175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
          180            185            190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
          195            200            205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
          210            215            220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
          225            230            235            240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
          245            250            255

```

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttcctcaaga gggcagcc 18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
 cttggcacca atgtccgaga ttcc 24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttg ccttg 45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 cgccgcgctc ccgcacccgc ggcccgcaca ccgcgcgct cccgcctctg caccgcgagc 60  
 ccggcggcct ccggcgcgga gcgagcagat ccagtcgggc ccgcagcgca actcggtcca 120  
 gtcggggcgcg ccgctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180  
 gcttgctgct ggccggcgcg gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240  
 ctccagtcaa gcccggcccc gctctcagct accgcagga ggaggccacc ctcaatgaga 300  
 tggtccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540  
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcgc 600  
 acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

```

gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
accagagggg ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840
tgtgcacacc cctgcccgtg gagggcgagc tttgccatga ccccgccagc cggcttctgg 900
acctcatcac ctgggagcta gagcctgatg gagccttgga ccgatgccct tgtgccagtg 960
gcctcctctg ccagcccccac agccacagcc tgggtgatgt gtgcaagccg accttcgtgg 1020
ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gagtatgaag 1080
ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
aagagatggc gctggggggag cctgcccgtg ccgccgctgc actgctggga ggggaagaga 1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260
gggtgtgtgt ttaggcgtgg gctgaccagg cttcttctta catcttcttc ccagtaagtt 1320
tcccctctgg cttgacagca tgaggtgttg tgcatgtgtt cagctcccc aggtgtttct 1380
ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaactgca ggagcagttt 1440
gccaccctg tccagattat tggctgcttt gcctctacca gttggcagac agcctgttgt 1500
tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaaccatc aacctggcaa 1620
aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
gtgttgctca gctcctacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
tctctcagca cagcctgggg aggggggtcat tgttctcttc gtccatcagg gatctcagag 1860
gctcagagac tgcaagctgc ttgcccaggt cacacagcta gtgaagacca gagcagtttc 1920
atctggttgt gactctaagc tcagtgtctt ctccactacc ccacaccagc cttggtgcca 1980
ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
attaaggtca aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
gttctcacag tgtgggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacagggttaa 2220
cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520
aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa 2586

```

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

```

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
  1              5              10              15

```

```

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
          20              25              30

```

```

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
    35              40              45

```

```

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50              55              60

```

```

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
    65              70              75              80

```

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
 85 90 95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
 100 105 110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
 115 120 125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
 130 135 140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
 145 150 155 160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
 165 170 175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
 180 185 190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
 195 200 205  
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
 210 215 220  
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
 225 230 235 240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
 245 250 255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
 260 265 270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
 275 280 285  
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
 290 295 300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
 305 310 315 320  
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
 325 330 335  
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile  
 340 345 350

&lt;210&gt; 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 237  
 ggagctgcac cccttgc 17  
  
 <210> 238  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 238  
 ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 239  
 gcagagcgga gatgcagcgg ctg 24  
  
 <210> 240  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 240  
 ttggcagctt catggagg 18  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 241  
 cctgggcaaa aatgcaac 18

<210> 242  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

<400> 244  
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50  
 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100  
 cactctcctt ccctcccaaa cacacatgtg catgtacaca cacacatata 150  
 cacacatata ccttcctctc cttcactgaa gactcacagt cactcactct 200  
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggccctggcc 250  
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300  
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350  
 tgagcagatc acttgaggtc aggagttcga gaccagcctg gccaacatgg 400  
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450  
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500  
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550  
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650  
 ccagggtctgc ccctgatggg gcctggcaat gactgagcag gccagcccc 700  
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750  
 gtgtagaatg actgccctgg gaggggtggtt ccttgggccc tggcagggtt 800  
 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850  
 gtgaatggtc ccctgccctg cagctccacc atgaggttct tcgtggcccc 900  
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtac 950  
 cctggcatgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000  
 tatacgcccc gctcgtccta ccgcgagget accactgtgg actgcaatga 1050  
 cctattcctg acggcagtc ccccggaact ccccgaggc acacagacct 1100  
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150  
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200  
 tgcccagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250  
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggtg 1300  
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcacgc 1350  
 cccaggggc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400  
 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccccaac 1450  
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500  
 gaacttccgg cccctggcca acctgcgtag cctggtgcta gcaggcatga 1550  
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600  
 agcctctcct tctatgacaa ccagctggcc cgggtgcccc ggcgggcaact 1650  
 ggaacaggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700  
 agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750  
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctgg 1800  
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850  
 ccttcatcca cccccgcgc ttccaccacc tgccccagat ggagaccctc 1900  
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagt 1950

cctgcccac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000  
 actgtgtcat ccgctgggcc aatgccacgg gcacccgtgt ccgcttcac 2050  
 gagccgcaat ccaccctgtg tgcggagcct ccggacctcc agcgcctccc 2100  
 ggtccgtgag gtgcccttcc gggagatgac ggaccactgt ttgccctca 2150  
 tctccccacg aagcttcccc ccaagcctcc aggtagccag tggagagagc 2200  
 atggtgctgc attgccgggc actggccgaa ccogaacccg agatctactg 2250  
 ggtcactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300  
 accgggtgta ccccgagggg accctggagc tgcggagggg gacagcagaa 2350  
 gaggcagggc tatacacctg tgtggcccag aacctggtgg gggctgacac 2400  
 taagacggtt agtgtggttg tgggccgtgc tctcctccag ccaggcaggg 2450  
 acgaaggaca ggggctggag ctccgggtgc aggagacca cccctatcac 2500  
 atcctgctat cttgggtcac cccacccaac acagtgtcca ccaacctcac 2550  
 ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600  
 gcctgcctcg ggaaccac agctacaaca ttaccgcct ccttcaggcc 2650  
 acggagtact gggcctgcct gcaagtggcc tttgctgatg cccacacca 2700  
 gttggcttgt gtatgggcca ggaccaaaga ggccacttct tgccacagag 2750  
 ccttagggga tcgtcctggg ctcatgcca tctggetct cgtgtcctt 2800  
 ctctggcag ctgggctagc ggcccacctt ggcacaggcc aaccaggaa 2850  
 ggggtgtggg gggaggcggc ctctccctcc agcctgggct ttctggggct 2900  
 ggagtgtccc ttctgtccgg gttgtgtctg ctccctcgt cctgccctgg 2950  
 aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000  
 accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050  
 atcactagga ctacttttta ccaaaagaga agcagtctgg gccagatgcc 3100  
 ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctgggc 3150  
 caagacagat ggggctttgt ggccctgggg gtgcttctgc agccttgaaa 3200  
 aagttgccct tacctcctag ggtcacctct gctgccattc tgaggaacat 3250

ctccaaggaa caggagggac tttggctaga gcctcctgcc tccccatctt 3300  
ctctctgccc agaggctcct gggcctggct tggctgtccc ctacctgtgt 3350  
ccccgggctg cacccttccc tcttctcttt ctctgtacag tctcagttgc 3400  
ttgctcttgt gcctcctggg caagggtga aggaggccac tccatctcac 3450  
ctcggggggc tgccctcaat gtgggagtga cccagccag atctgaagga 3500  
catttgggag agggatgccc aggaacgcct catctcagca gcctgggctc 3550  
ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600  
atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650  
aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
				155					160					165	
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	
				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
				185					190					195	
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
				200					205					210	
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
				215					220					225	
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
				230					235					240	
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
				245					250					255	
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	
				260					265					270	
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
				275					280					285	
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	
				290					295					300	
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
				305					310					315	
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	
				320					325					330	
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
				335					340					345	
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	
				350					355					360	
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
				380					385					390	
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
				395					400					405	
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	

	410		415		420
Leu Pro Leu Ile	Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val			
	425		430		435
Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu			
	440		445		450
Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu			
	455		460		465
Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly			
	470		475		480
Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr			
	485		490		495
Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val			
	500		505		510
Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu			
	515		520		525
Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His			
	530		535		540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn			
	545		550		555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr			
	560		565		570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr			
	575		580		585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala			
	590		595		600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr			
	605		610		615
Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly			
	620		625		630
Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly			
	635		640		645
Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly			
	650		655		660
Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser			
	665		670		675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser  
710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgatcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag ggcgtgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcctcctcat catctgtctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
accgcaccta ccgctgtgcc caccctctgg ccacactctt caagatcctg 250  
gcgtccttct acatcagcct agtcactctt tacggcctca tctgcatgta 300  
cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350  
cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400  
ttcgcttca tgctgcacct cattgaccaa tacgacccgc tctactccaa 450  
gcgcttcgcc gtcttcctgt cggagggtgag tgagaacaag ctgcggcagc 500  
tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550  
aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600  
ccctgacact gtgtttgacc tggaggagct ggaggctctc aagctggagc 650  
tgatccccga cgtgaccatc ccgcccagca ttgcccagct cacgggcctc 700  
aaggagctgt ggctctacca cacagcggcc aagattgaag cgctgcgct 750  
ggccttcctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800  
tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850  
cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900  
cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950  
taagcaagct gccacagggtg gtcacagatg tgggcgtgca cctgcagaag 1000  
ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050  
gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100  
gcatccccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150  
aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200  
gcaccgctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250  
ccatccagat cggcaacctc accaacctgg agcgctctta cctgaaccgc 1300  
aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350  
ctacctggac ctgagccaca acaacctgac ctctctccct gccgacatcg 1400  
gcctcctgca gaacctccag aacctagcca tcacggccaa ccggatcgag 1450

acgctccctc cggagctctt ccagtgcggg aagctgcggg ccctgcacct 1500  
 gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550  
 acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600  
 gagctgggcg agtgcccact gctcaagcgc agcggcttgg tggaggagga 1650  
 ggacctgttc aacacactgc caccgcaggt gaaggagcgg ctgtggaggg 1700  
 ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750  
 gaccgctgcc cagtcctcag gcccgagggg gcaggcctag cttctcccag 1800  
 aactcccga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850  
 gcttgtgagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900  
 ttttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950  
 agcaagtctc aagagcgcag tatttgata atcagggtct cctccctgga 2000  
 ggccagctct gcccagggg ctgagctgcc accagaggtc ctgggacct 2050  
 cactttagtt cttggtattt atttttctcc atctcccacc tccttcatcc 2100  
 agataactta tacattccca agaaagttca gccagatgg aaggtgttca 2150  
 gggaaaggtg ggctgccttt tcccctgtc cttatttagc gatgccgccg 2200  
 ggcatttaac acccacctgg acttcagcag agtgggccgg ggcgaaccag 2250  
 ccatgggacg gtcaccagc agtgccgggc tgggctctgc ggtgcgggtc 2300  
 acgggagagc aggcctccag ctggaaaggc caggcctgga gcttgctct 2350  
 tcagtttttg tggcagtttt agttttttgt tttttttttt tttaatcaaa 2400  
 aaacaatttt ttttaaaaaa aagctttgaa aatggatggt ttgggtatta 2450  
 aaaagaaaaa aaaaacttaa aaaaaaaaag acactaacgg ccagtgagtt 2500  
 ggagtctcag ggcagggtgg cagtttccct tgagcaaagc agccagacgt 2550  
 tgaactgtgt ttcctttccc tgggcgcagg gtgcagggtg tcttccggat 2600  
 ctggtgtgac cttggtccag gagttctatt tgttctctgg gagggagggt 2650  
 tttttgtttg ttttttgggt ttttttgggt tcttgttttc tttctcctcc 2700  
 atgtgtcttg gcaggcactc atttctgtgg ctgtcggcca gagggaatgt 2750  
 tctggagctg ccaaggaggg aggagactcg ggttggctaa tccccgatg 2800

aacggtgctc cattcgccacc tccccctcctc gtgcctgccc tgcctctcca 2850  
 cgcacagtgt taaggagcca agaggagcca cttegccag actttgtttc 2900  
 cccacctcct gcggcatggg tgtgtccagt gccaccgctg gcctccgctg 2950  
 cttccatcag ccctgtcgcc acctggctcct tcatgaagag cagacactta 3000  
 gaggttggtc gggaatgggg aggtcgcccc tgggagggca ggcgttggtt 3050  
 ccaagccggt tcccgtccct ggcgccctgga gtgcacacag cccagtcggc 3100  
 acctgggtggc tggaagccaa cctgcttttag atcactcggg tccccacctt 3150  
 agaagggtcc ccgccttaga tcaatcacgt ggacactaag gcacgtttta 3200  
 gagtctcttg tcttaatgat tatgtccatc cgtctgtccg tccatttgtg 3250  
 ttttctgcgt cgtgtcattg gatataatcc tcagaaataa tgcacactag 3300  
 cctctgacaa ccatgaagca aaaatccggtt acatgtgggt ctgaacttgt 3350  
 agactcggtc acagtatcaa ataaaatcta taacagaaaa aaaaaaaaaa 3400  
 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
			20						25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
			35						40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
			50						55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
			65						70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
			80						85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

95										100					105				
Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro					
				110					115					120					
Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu					
				125					130					135					
Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp					
				140					145					150					
Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu					
				155					160					165					
Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp					
				170					175					180					
Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val					
				185					190					195					
Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu					
				200					205					210					
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala					
				215					220					225					
Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp					
				230					235					240					
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu					
				245					250					255					
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr					
				260					265					270					
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu					
				275					280					285					
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp					
				290					295					300					
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr					
				305					310					315					
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr					
				320					325					330					
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser					
				335					340					345					
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn					
				350					355					360					

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

caacaatgag ggcaccaagc 20

&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50  
 gcgctctccc gtcccgcggt ggttgcctgt gctgccgctg ctgctggggc 100  
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250  
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300  
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctgget 350  
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400  
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatgggtggc 450  
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500  
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550  
 cagctggcat tgggtctagag ctttataagg ccattcagcg agggaccatc 600  
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650  
 tgattcgggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750  
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800  
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850  
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900  
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950  
agatgcctta agccagctca tgaatggccc catcagaaaag aagctcaaaa 1000  
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050  
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100  
gctggaggca gggatcaacg tgacgggtga taatggacag ctggatctca 1150  
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200  
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250  
taaactcttg gaaacatctg cttttgtcaa gtccatacag aaccttgctt 1300  
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350  
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400  
gggctggaga tgagctgggt tggccttggg gcacagagct gagctgaggc 1450  
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500  
gatcaagaag gttctgacca gcttctgcag aggataaaaat cattgtctct 1550  
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tggggtgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgaacc tgctcagcca ccgctgggca 250

ctcagggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300

cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```

<210> 257
<211> 314
<212> PRT
<213> Homo Sapien

<400> 257
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
  1             5             10             15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
             20             25             30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
             35             40             45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
             50             55             60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
             65             70             75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
             80             85             90

```

Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	
				95					100					105	
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	
				110					115					120	
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	
				125					130					135	
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	
				140					145					150	
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	
				155					160					165	
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	
				170					175					180	
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	
				185					190					195	
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	
				200					205					210	
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	
				215					220					225	
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	
				230					235					240	
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	
				245					250					255	
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	
				260					265					270	
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	
				275					280					285	
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	
				290					295					300	
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		
				305					310						

&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

cctcctaggg ctctttgccc tcatectctc tggcaaagtgc agttacagcc 100  
 cggagcccgga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150  
 cgtgctggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200  
 gaatgtggaa agactctcgg agctgggtgca ggctgtgtcg gatcccagct 250  
 ctctcaata cggaaaatac ctgaccctag agaagtgtggc tgatctggtg 300  
 aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450  
 cactatgtgg gaggacctac ggaaacccat gttgtaaggc cccacatcc 500  
 ctaccagctt ccacaggcct tggccccca tgtggacttt gtggggggac 550  
 tgcaccgttt tcccccaaca tcacccctga ggcaacgtcc tgagccgcag 600  
 gtgacagga ctgtaggcct gcacctgggg gtaacccct ctgtgatccg 650  
 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
 acagccaagc ctgtgcccag ttctggagc agtatttcca tgactcagac 750  
 ctggctcagt tcatgcgcct cttcgggtggc aactttgcac atcaggcatc 800  
 agtagcccg gtggttgac aacagggccg gggccgggccc gggattgagg 850  
 ccagtctaga tgtgcagtac ctgatgagt ctggtgccaa catctccacc 900  
 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950  
 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000  
 tgagctatgg agatgatgag gactccctca gcagcgcta catccagcgg 1050  
 gtcaacactg agctcatgaa ggctgccgct cggggtctca ccctgctctt 1100  
 cgctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
 agttccgccc taccttcctt gcctccagcc cctatgtcac cacagtggga 1200  
 ggcacatcct tccaggaacc tttctcatc acaaatgaaa ttgttgacta 1250  
 tatcagtggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
 aggaagctgt aacgaagttc ctgagctcta gccccacct gccaccatcc 1350  
 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtgggtca gcaacagagt gcccattcca tgggtgtccg 1450  
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500  
 gagcacagga tccttagtgg ccgccccccct cttggctttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650  
 cctggctggg atcctgtaac aggtctggga acaccaactt cccagctttg 1700  
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750  
 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctggtgga 1800  
 agccctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aacctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900  
 atcatactca ggtctcccta ctctgcctt agattcctca ataagatgct 1950  
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000  
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttactgcaa ggagacctct actgtcaccg 2100  
 tttactcttt cctaccctga catccagaaa caatggctc cagtgcatac 2150  
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttcctc 2250  
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300  
 tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1						5			10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser	Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met	Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His Val His Thr Val Ser	Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg	Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu	Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser	Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr	Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile	Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly Gly Gly Phe Ser Asn	Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe	Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala	Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr	Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr	Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn	Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn	Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr	Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln	Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly	Thr Pro Thr Ser Gln Leu	545	550	555

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

```

gccgcgcgct ctctcccggc gcccacacct gtctgagcgg cgcagcgagc 50
cgcgggcccgg gcgggctgct cggcgcgga cagtgtcgg catggcaggg 100
attccagggc tcctcttctt tctcttcttt ctgtctgtg ctgttgggca 150
agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaact ccactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
gtgaagttaa ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcctaaagc ccaagttaa agatggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgtcttacc agcaatgcga tgcccagcca ggggccagcg ggtctgggg 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

```

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200  
 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
 ttccctcctg gcagcaatta agggctcttca tggtcttatt ttaggagagg 1300  
 ccaaattggt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400  
 tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450  
 ttttaagcagt ttgaaggcat acttttgcac agaaataaaaa aaaataactga 1500  
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550  
 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	20	25	30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262  
 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

<400> 262  
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50  
 ccatgggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100  
 accttcacct cctgctgct gctggcgtcg acagccatcc tcaatgcggc 150  
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200  
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
 atccagaaga atgggacca cactgcgca ggttctctgc tcaccagccg 300  
 ctgggtgatc actgctgcc actgtttcaa ggacaacctg aacaaaccat 350  
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
 cgggccaga aggtgggtgt tgctgggtg gagccccacc ctgtgtattc 450  
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctgagcgt 500  
 ccatacagtt ctgagagcg gtctgccca tctgcctacc tgatgcctct 550  
 atccacctcc ctccaaacac cactgctgg atctcaggct gggggagcat 600  
 ccaagatgga gttcccttgc cccacctca gacctgcag aagctgaagg 650  
 ttctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700  
 ggacagggac ccactactga ggacatgctg tgtgccggct acttgagg 750  
 ggagcgggat gcttgtctg gcgactcgg gggccccctc atgtgccagg 800  
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggtgt 850  
 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccgctc 900  
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgtcagg 950  
 ggggtggggc cctcaggga ccgagccagg gctctggggc cgccgcgcgc 1000  
 tctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050  
 cacatctgga tctggatctg cggcgccctc gggcggttcc cccgcccgt 1100  
 aataggctca tctacctca cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc cctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttcggc 1250  
cccgcccccg gggcccagcg cttttgtgta tataaatgtt aatgattttt 1300  
ataggtattt gtaaccctgc ccacatatct tattttattcc tccaatttca 1350  
ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gtgc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 266  
 agctctagac caatgccagc ttcc 24  
  
 <210> 267  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 267  
 gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45  
  
 <210> 268  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 268  
 ggggaattca ccctatgaca ttgcc 25  
  
 <210> 269  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 269  
 gaatgccctg caagcatcaa ctgg 24  
  
 <210> 270  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 270  
 gcacctgtca cctacactaa acacatccag cccatctgtc tccaggctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtagac cccg 24

<210> 275  
<211> 45  
  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
gggcagggat tccagggctc c 21

<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcacgcatt gctggtagag caag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tgggtggagct gcacaacctc taccgggccc 150  
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250  
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
 tacaacctca gcgcccac ctgcagccca ggccagatgt gcggccacta 400  
 cacgcagggtg gtatgggcca agacagagag gatcggtgt ggttcccact 450  
 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500  
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600  
 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700  
 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750  
 cagaggtctc aggtccctg gcaaccaagg ctctgcctgc tgtggaaacc 800  
 caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850  
 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900  
 gectgcctc cttggatgag gagccagtta cttccccaa atcgacccat 950  
 gttcctatcc caaaatcagc agacaaagt acagacaaaa caaaagtgcc 1000  
 ctctaggagc ccagagaact ctctggacct caagatgtcc ctgacagggg 1050  
 caagggaact cctaccccat gccagaggg aggctgaggc tgaggctgag 1100  
 ttgcctcctt ccagtgaggt cttggcctca gttttccag ccagggacaa 1150  
 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200  
 agtccttccc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250  
 gggcgtgccc tggtctgca gtcgtccttg ccagggtgag agggccctga 1300  
 caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350  
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

ttctgaatgg gataccactc aaaggggtgaa gaggtcagct gtcctcctgt 1450  
 catcttcccc accctgtccc cagccccctaa acaagatact tcttggttaa 1500  
 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600  
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650  
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700  
 tgccacaca gcatgtgcgc tctccctgag tgccctgtga gctggggatg 1750  
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800  
 tgagtggggg aggcagggac gaggggaagga aagtaactcc tgactctcca 1850  
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu	140	145	150
Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr	155	160	165
Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly	170	175	180
Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser	185	190	195
Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro	200	205	210
Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser	215	220	225
Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile	230	235	240
Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys	245	250	255
Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr	260	265	270
Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr	275	280	285
Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu	290	295	300
Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile	305	310	315
Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser	320	325	330
Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly	335	340	345
Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu	350	355	360
Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro	365	370	375
Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr	380	385	390
Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser	395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tcattctcca agttatggtg gacgtacttc tgttggtctc cctctgcttg 100  
 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150  
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200  
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250  
 attacacttc tctccttggc tggaacagg attggtgaaa tactccctga 300  
 acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350  
 atatttcaga gctccaaact gcatttcag ccctacagct caaatatctg 400  
 tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450  
 tttggccaac acactccttg tgtaaagct gaacaggaac cgaatctcag 500  
 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550  
 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600  
 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
 atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700  
 aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750  
 gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800  
 cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
 ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900  
 actgcacatt gggaacaaca gagtacgcta cattgctgat tgtgccttcc 950  
 gggggccttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000  
 tggactattg aagacatgaa tggtgcttcc tctgggcttg acaaactgag 1050  
 gcgactgata ctccaaggaa atcgatccg ttctattact aaaaaagcct 1100  
 tcaactggtt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150  
 atgtctttac aaggcaatgc attttcacaa atgaagaaac tgcaacaatt 1200  
 gcatttaaat acatcaagcc ttttggtgca ttgccagcta aaatggctcc 1250  
 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300  
 gccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggttttggtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400  
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450  
 gccagcagca gtgattcccc aatgactttt gcttggaata aagacaatga 1500  
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggccaag 1550  
 gtggcgaggt gatggagtat accaccatcc ttgggtgctg cgaggtggaa 1600  
 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650  
 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700  
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750  
 gagtgtgctg ctgtggggca cccagcccc cagatagcct ggcagaagga 1800  
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850  
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900  
 gtatacagct gcacagctca gaacagtgc ggaagtatct cagcaaattgc 1950  
 aactctgact gtcctagaaa caccatcatt tttgcggcca ctgttgacc 2000  
 gaactgtaac caaggagaa acagccgtcc tacagtgcac tgctggagga 2050  
 agccctcccc cttaaactgaa ctggacaaa gatgatagcc cattggtggg 2100  
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150  
 actcagatgt cagtgatgct gggaaataca catgtgagat gtctaacc 2200  
 cttggcactg agagaggaaa cgtgctgctc agtgtgatcc cactccaac 2250  
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300  
 ccactgtggg tgtcgtgatc atagccgtgg tttgctgtgt ggtgggcacg 2350  
 tcactcgtgt ggggtggtcat catataccac acaaggcgga ggaatgaaga 2400  
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450  
 gttatttgct atctcaggga acgttagctg acaggcagga tgggtacgtg 2500  
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550  
 atttttctta ccacaacatg acagtagtgg gacctgccat attgacaata 2600  
 gcagtgaagc tgatgtggaa gctgccacag atctgttctt ttgtccgttt 2650  
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata caggttgcag tcctgacca agaacagttt 2750  
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctacca 2800  
 tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatac 2850  
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900  
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950  
 agtgcaaadc cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000  
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050  
 ttggacagcc atcagattgt cagccaagag cctttttattt gaaagctcat 3100  
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150  
 agattttcag gaagaaaadc acatttgtac ctttaaacag actttagaaa 3200  
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250  
 tgagaccaaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300  
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350  
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400  
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450  
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500  
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550  
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600  
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650  
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25				30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

	290		295		300
Leu Lys Thr	Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr	Ile		
	305		310		315
Glu Asp Met Asn	Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg	Arg		
	320		325		330
Leu Ile Leu Gln	Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys	Ala		
	335		340		345
Phe Thr Gly Leu	Asp Ala Leu Glu His	Leu Asp Leu Ser Asp	Asn		
	350		355		360
Ala Ile Met Ser	Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys	Lys		
	365		370		375
Leu Gln Gln Leu	His Leu Asn Thr Ser	Ser Leu Leu Cys Asp	Cys		
	380		385		390
Gln Leu Lys Trp	Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe	Gln		
	395		400		405
Ser Phe Val Asn	Ala Ser Cys Ala His	Pro Gln Leu Leu Lys	Gly		
	410		415		420
Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp	Asp		
	425		430		435
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser	Ala		
	440		445		450
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser	Ser		
	455		460		465
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu	Leu		
	470		475		480
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala	Gln		
	485		490		495
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg	Glu		
	500		505		510
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser	Asn		
	515		520		525
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val	Asn		
	530		535		540
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile	Arg		
	545		550		555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560	565		570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575	580		585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590	595		600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605	610		615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620	625		630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665	670		675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740	745		750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 815 820 825  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
 1025 1030 1035  
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
 1040 1045 1050  
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
 1055

<210> 291  
 <211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50

ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100

tggaaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150

gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200

acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250

ttggtgtggt ctgacataaa taaataatct taaagcagct gttccccctcc 300

ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350

agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400

gatatttttg gaatgaaaag tttggggcctt ttttagtaaa gtaaagaact 450

ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500

aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550

gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600

tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650

ttcatcaacc tccttttttt taaattttta ttctttttgg tatcaagatc 700

atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800

ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850

ataggtccta ggtttaacag ggccctatct gacccctgc ttgtggtgct 900

gctggctctt caacttcttg tgggtggtgg tctggtgcgg gctcagacct 950

gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000

cggaaaaacc tgcgtgaggt tccgatggc atctccacca acacacggct 1050

gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100

agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150

accattgaaa ttggggcttt caatggctctg gcgaacctca acactctgga 1200

actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```

tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300  
 ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350  
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggctctgt 1400  
 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450  
 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500  
 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550  
 aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600  
 gacaaccttc agtcactagt ggagatcaac ctggcacaca ataataaac 1650  
 attactgctt catgacctct tcaactccctt gcatcatcta gagcggatac 1700  
 atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750  
 tgggtggataa aagacatggc cccctcgaac acagcttggt gtgcccgggtg 1800  
 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850  
 attacttcac atgctatgct ccggtgattg tggagcccc tgcagacctc 1900  
 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950  
 cctgacatct gtatcttggg ttactccaaa tggaacagtc atgacacatg 2000  
 gggcgtacaa agtgccgata gctgtgctca gtgatggtac gttaaatttc 2050  
 acaaagttaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100  
 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150  
 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200  
 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250  
 agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300  
 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350  
 agtgggatcc caggaattga tgaggatcatg aagactacca aaatcatcat 2400  
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450  
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500  
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550

catggaaagc cacctgcccc tgcttgctat cgagcatgag cacctaaatc 2600  
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650  
 ataaattcaa tacacagttc agtgcattgaa ccgttattga tccgaatgaa 2700  
 ctctaaagac aatgtacaag agactcaaatt ctaaaacatt tacagagtta 2750  
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800  
 tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850  
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900  
 caaaaa 2906

<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
1				5					10					15
Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

	155		160		165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp	335		340		345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

agccgacgct gctcaagctg caactctgtt gcagttggca gttcttttcg 50

gtttccctcc tgetgtttgg gggcatgaaa gggcttcgcc gccgggagta 100  
 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150  
 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200  
 gcgcgcgctg ggagcttcgg gtagagacct aggcgcgtgg accgcgatga 250  
 gcgcgcgag cctccgtgag cgcgcgcgg ggttggggct gctgctgtgc 300  
 gcggtgctgg ggcgcgtgg ccggtccgac agcggcggtc gcggggaact 350  
 cgggcagccc tctggggtag ccgcgcgag cccatgcccc actacctgcc 400  
 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450  
 cccgagccac tcccgctctg ggctcgtcgg ctggacttaa gtcacaacag 500  
 attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550  
 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600  
 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650  
 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700  
 ttagcagcaa caatatctca gagctccaaa ctgcatttcc agccctacag 750  
 ctcaaatact tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800  
 gtatcttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850  
 accgaatctc agctatcca cccaagatgt ttaaaactgcc ccaactgcaa 900  
 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950  
 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000  
 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050  
 cagctggacc ataacaacct aacagagatt accaaaaggct ggctttacgg 1100  
 cttgctgatg ctgcaggaac ttcatctcag ccaaaatgcc atcaacagga 1150  
 tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200  
 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250  
 cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300  
 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

aatgaaat t t cctggactat tgaagacatg aatgggtgctt tctctgggct 1400  
tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450  
ctaaaaaagc cttcactggg ttggatgcat tggagcatct agacctgagt 1500  
gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550  
actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600  
taaaatggct cccacagtgg gtggcgga aaactttca gagctttgta 1650  
aatgccagtt gtgcccattc tcagctgcta aaaggaagaa gcatttttgc 1700  
tgtagccca gatggctttg tgtgtgatga ttttcccaa cccagatca 1750  
cggttcagcc agaaacacag tcggcaataa aaggttcaa tttgagttc 1800  
atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850  
aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900  
tccgggcccc aggtggcgag gtgatggagt ataccaccat ccttcggctg 1950  
cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctcaa 2000  
tcactttggg tcactctact ctgtcaaagc caagcttaca gtaaatatgc 2050  
ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100  
atggcacgct tggagtgtgc tgctgtgggg caccagccc cccagatagc 2150  
ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200  
tgcatgtgat gcccaggat gacgtgttct ttatcgtgga tgtgaagata 2250  
gaggacattg gggatacag ctgcacagct cagaacagtg caggaagtat 2300  
ttcagcaaat gcaactctga ctgtcctaga aacaccatca ttttgcggc 2350  
cactgttggg ccgaactgta accaaggag aaacagccgt cctacagtgc 2400  
attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450  
cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500  
tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550  
atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600  
ccccactcca acctgcgact ccctcagat gacagcccca tcgttagacg 2650  
atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgcgtg 2700

gtggtgggca cgtcactcgt gtgggtgggc atcatatacc acacaaggcg 2750  
 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800  
 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850  
 gatgggtacg tgtcttcaga aagtgggaag caccaccagt ttgtcacatc 2900  
 ttcaggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950  
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000  
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050  
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100  
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150  
 gagtgctacc catgttctca tccttcagaa gaatcctgcg aacggagctt 3200  
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250  
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300  
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350  
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400  
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450  
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500  
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550  
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600  
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650  
 aacttttatt taaaagagag agaattctat gttttttaaa tggagttatg 3700  
 aatttttaaaa ggataaaaaat gctttattta tacagatgaa ccaaaattac 3750  
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800  
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850  
 aaattaatga tataaatcat gattattttta tgtattttta taatgccaga 3900  
 tttcttttta tggaaaatga gttactaaag catttttaaat aataacctgc 3950  
 ttgtaccatt ttttaaatag aagttacttc attatatttt gcacattata 4000

aaa 4053

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu  
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

	215		220		225
Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala				
230	235				240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met					
245	250				255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu					
260	265				270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly					
275	280				285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn					
290	295				300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu					
305	310				315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser					
320	325				330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn					
335	340				345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser					
350	355				360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile					
365	370				375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg					
380	385				390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala					
395	400				405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn					
410	415				420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys					
425	430				435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys					
440	445				450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln					
455	460				465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly					
470	475				480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln	740	745	750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
 755 760 765  
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
 770 775 780  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
 785 790 795  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
 800 805 810  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
 815 820 825  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 830 835 840  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
 845 850 855  
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
 860 865 870  
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
 875 880 885  
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 890 895 900  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 905 910 915  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 920 925 930  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 935 940 945  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 950 955 960  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 965 970 975  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 980 985 990  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 995 1000 1005  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

<400> 297  
ggctggagac actgaacct 19

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 298  
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 299  
cattcccagt ataaaaattt tc 22

<210> 300  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 300  
gggtcttggt gaatgagg 18

<210> 301  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 301  
gtgcctctcg gttaccacca atgg 24

<210> 302  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 302

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 303

gcctttgaca accttcagtc actagtgg 28

<210> 304

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 304

cccatgtgt ccatgactgt tccc 24

<210> 305

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 306

actccaagga aatcgatcc gtcc 24

<210> 307

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

ttagcagctg aggatgggca caac 24

<210> 308

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 308

actccaagga aatcggatcc gttc 24

<210> 309

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 309

gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcccagct tgacttgaat ggaaggagcc 50

cgagcccgcg gagcgcagct gagactgggg gagcgcgttc ggccctgtggg 100

gcgccgctcg gcgccggggc gcagcaggga aggggaagct gtggtctgcc 150

ctgctccacg aggcgccact ggtgtgaacc gggagagccc ctgggtggtc 200

ccgtccccta tccctccttt atatagaaac cttccacact gggaaggcag 250

ggcgaggca ggagggctca tggtagcaa ggaggccggc tgatctgcag 300

gcgcacagca ttccgagttt acagatTTTT acagatacca aatggaaggc 350

gaggaggcag aacagcctgc ctggttccat cagccctggc gccagggcgc 400

atctgactcg gcacccctg caggcaccat ggcccagagc cgggtgctgc 450  
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500  
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550  
 agagaacgaa tttgcggagg aggagccggt gctggtactg agccctgagg 600  
 agcccgggccc tggcccagcc gcggtcagct gccccgaga ctgtgcctgt 650  
 tcccaggagg gcgtcgtgga ctgtggcggg attgacctgc gtgagttccc 700  
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccagc 750  
 tggaaaagat ctacctgag gagctctccc ggctgcaccg gctggagaca 800  
 ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850  
 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900  
 tgaccttggc accccgcttc ctgccaaacg ccctgatcag tgtggacttt 950  
 gctgccaaact atctcaccaa gatctatggg ctacaccttg gccagaagcc 1000  
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050  
 tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100  
 tccagcaact tctgcgcca cgtgcccag cacctgccgc ctgccctgta 1150  
 caagctgcac ctcaagaaca acaagctgga gaagatcccc ccggggggcct 1200  
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250  
 actgacgagg gcctggacaa cgagaccttc tggaagctct ccagcctgga 1300  
 gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350  
 cgcgagcct ggtgctgctg cacttggaga agaacgccat ccggagcgtg 1400  
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450  
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500  
 tcaagcgggt gcacacggtg cacctgtaca acaacgcgct ggagcgcgtg 1550  
 cccagtggcc tgctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600  
 gatcacaggc attggccgcg aagactttgc caccacctac ttctggagg 1650  
 agctcaacct cagctacaac cgcatacca gccacaggt gcaccgcgac 1700

gccttcgcga agctgcgcct gctgcgctcg ctggacctgt cgggcaaccg 1750  
 gctgcacacg ctgccacctg ggctgcctcg aaatgtccat gtgctgaagg 1800  
 tcaagcgcaa tgagctggct gccttggcac gaggggctcg ggcgggcatg 1850  
 gctcagctgc gtgagctgta cctcaccagc aaccgactgc gcagccgagc 1900  
 cctgggcccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950  
 tcgccgggaa tcagctcaca gagatccccg aggggctccc cgagtcactt 2000  
 gagtacctgt acctgcagaa caacaagatt agtgcggtgc ccgccaatgc 2050  
 cttcgactcc acgccccacc tcaaggggat ctttctcagg tttaacaagc 2100  
 tggctgtggg ctccgtgggtg gacagtgcct tccggaggct gaagcacctg 2150  
 caggtcttgg acattgaagg caacttagag tttggtgaca ttccaagga 2200  
 ccgtggccgc ttggggaagg aaaaggagga ggaggaagag gaggaggagg 2250  
 aggaagagga aacaagatag tgacaagggtg atgcagatgt gacctaggat 2300  
 gatggaccgc cggactcttt tctgcagcac acgcctgtgt gctgtgagcc 2350  
 cccactctg ccgtgctcac acagacacac ccagctgcac acatgaggca 2400  
 tcccacatga cacgggctga cacagtctca tatccccacc ccttccccacg 2450  
 gcgtgtccca cggccagaca catgcacaca catcacacc tcaaacaccc 2500  
 agctcagcca cacacaacta cctccaaac caccacagtc tctgtcacac 2550  
 cccactacc gctgccacgc cctctgaatc atgcagggaa gggctctgcc 2600  
 ctgccctggc acacacaggc acccattccc tccccctgct gacatgtgta 2650  
 tgcgatatga tacacaccac acacacacac atgcacaagt catgtgcgaa 2700  
 cagccctcca aagcctatgc cacagacagc tcttgcccca gccagaatca 2750  
 gccatagcag ctgcgcgtct gcctgtcca tctgtccgtc cgttccttgg 2800  
 agaagacaca agggatatca tgctctgtgg ccagggtgcct gccaccctct 2850  
 ggaactcaca aaagctgggt tttattcctt tcccatccta tggggacagg 2900  
 agccttcagg actgctggcc tggcctggcc caccctgctc ctccagggtg 2950  
 tgggcagtca ctctgctaag agtccctccc tgccacgccc tggcaggaca 3000  
 caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100  
 ctgggctgag ccagggagga aggacccagc tgcacctagg agacaccttt 3150  
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200  
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250  
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 311

gcattggccg cgagactttg cc 22

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 312

gcggccacgg tccttgaaa tg 22

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 313

tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314

<211> 3003

<212> DNA

<213> Homo Sapien

<400> 314

gggagggggc tccgggcgcc gcgcagcaga cctgctccgg ccgcgcgcct 50

cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100

gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccaccc 150  
 caacctgttc ctgcgcgcgc actgcgctgc gcccaggac ccgctgcca 200  
 acatggattt tctcctggcg ctggtgctgg tctcctcgt ctacctgcag 250  
 gcggccgcgc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300  
 tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350  
 gccagtcttg gggacagtgt cagcctgtgt gccaaaccag atgcaaacat 400  
 ggtgaatgta tcgggccaaa caagtgcag tgtcatcctg gttatgctgg 450  
 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500  
 gtaagcacag gtgcataaac acttacggca gctacaagt ctactgtctc 550  
 aacggatata tgctcatgcc ggatgggtcc tgctcaagt ccctgacctg 600  
 ctccatggca aactgtcagt atggctgtga tgttgtaaa ggacaaatac 650  
 ggtgccagt cccatcccct ggctgcacc tggctcctga tgggaggacc 700  
 tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750  
 taggcaatgt gtcaaacactt ttgggagcta catctgcaag tgcataaag 800  
 gcttcgatct catgtatatt ggaggcaaat atcaatgtca tgacatagac 850  
 gaatgctcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900  
 cgtacgtggg tcctacaagt gcaaatgtaa agaaggatac caggggtgatg 950  
 gactgacttg tgtgtatct ccaaaagtta tgattgaacc ttcaggtcca 1000  
 attcatgtac caaagggaaa tggtagcatt ttaaagggtg acacaggaaa 1050  
 taataattgg attcctgatg ttggaagtac ttggtggcct ccgaagacac 1100  
 catatattcc tcctatcatt accaacaggc ctacttctaa gccaacaaca 1150  
 agacctacac caaagccaac accaattcct actccaccac caccaccacc 1200  
 cctgccaaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250  
 caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300  
 gggattacag ttgacaacag ggtacagaca gaccctcaga aaccagagg 1350  
 agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcactggga accaatcagg 1450  
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500  
 gggaaaagct gcacgcttgg tgctacctct cggccgcctc atgcattcag 1550  
 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600  
 acactccagg tgtttgtgag aaaacacggt gcccacggag cagccctgtg 1650  
 ggggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700  
 gggctgacat caagagcgaa tcacaaagat gattaaagggt ttggaaaaaa 1750  
 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800  
 agaagactga ggggcaaacc attgatgggt ttcaagtata tgaagggttg 1850  
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900  
 caagaggaaa ctggccttaga ctagagtata agggagcatt tcttggcagg 1950  
 ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000  
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggt 2050  
 taaagatggt cttaccaag gaaaagtaac aaattataga atttcccaa 2100  
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150  
 taatttggac aaggcttaat ttaggcattt ccctcttgac ctccaatgg 2200  
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250  
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300  
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350  
 cctagtgtgg cgggtggtttt caatgtttct tcatggtaaa ggtataagcc 2400  
 tttcatttgt tcaatggatg atgtttcaga tttttttttt ttttaagagat 2450  
 ctttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500  
 cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550  
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600  
 tcaattggac tctcccagggt tccacagaac agtaatatatt tttgaacaat 2650  
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700  
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750

gtagatccat ttttaatggg tcatttcctt tatgggcata taactgcaca 2800  
gctgaagatg aaaggggaaa ataaatgaaa attttacttt tcgatgccaa 2850  
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900  
catcttggtt attatttaat gttttctaaa ataaaaaatg ttagtggttt 2950  
tccaaatggc ctaataaaaa caattatttg taaataaaaa cactgttagt 3000  
aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

Met	Asp	Phe	Leu	Leu	Ala	Leu	Val	Leu	Val	Ser	Ser	Leu	Tyr	Leu	1	5	10	15
Gln	Ala	Ala	Ala	Glu	Phe	Asp	Gly	Arg	Trp	Pro	Arg	Gln	Ile	Val	20	25	30	
Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

Thr Cys Val Asp	Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys
170	175	180
Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
185	190	195
Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200	205	210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215	220	225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230	235	240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245	250	255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260	265	270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275	280	285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290	295	300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305	310	315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320	325	330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335	340	345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350	355	360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365	370	375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380	385	390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395	400	405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410	415	420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

	425		430		435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly					
	440		445		450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser					
	455		460		465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala					
	470		475		480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln					
	485		490		495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg					
	500		505		

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA

<213> Homo Sapien

<400> 319

```

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50
tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100
caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250
caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300
ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350
tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400
acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450
gttgatgatc ctgtcacaaa gccagtgggtg cagattcacc ctccctctgg 500
ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550
gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650
agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700
tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750
tatggacttc aagtgaattc tgataaaggg ctaaaagtag gggaaagtgtt 800
tactgttgac cttggagagg ccaccctatt tgattgttct gctgattctc 850
atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900
atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100
atcactattt ttgattatat ccatgtgtct tctcttccta tggaaaaaat 1150
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```

ottoggaata tatgaatttg ttgcttttcc agatgtttct ggtgtttcca 1300  
 ggattccaag caggtctggt ccagcctctg attgtgtatc ggggcaagat 1350  
 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
 agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450  
 ttctgaagaa acattttaag gaaaaacagt ggaaaagtat attaactctg 1500  
 aatcagttaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
 tgcagaatag aggcatttat gcaaattgaa ctgcagggtt ttcagcatat 1600  
 acacaatgtc ttgtgcaaca gaaaaacatg ttgggggaaat attcctcagt 1650  
 ggagagtcgt tctcatgctg acggggagaa cgaaagtgaac aggggtttcc 1700  
 tcataagttt tgtatgaaat atctctacaa acctcaatta gttctactct 1750  
 acactttcac tatcatcaac actgagacta tctgtctca cctacaaatg 1800  
 tggaaacttt acattgttcg atttttcagc agactttggt ttattaaatt 1850  
 tttattagtg ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900  
 ttctatcttg ttattgttac aacaaagtaa taaggatggg tgtcacaaaa 1950  
 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050  
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100  
 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
1				5					10					15

Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30

Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser		65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro		80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu		95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu		110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr		125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr		140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg		155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser		170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala		185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg		200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile		215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu		230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu		245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp		260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro		275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp		290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu		305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu				

	320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly	335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp	350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly	365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His	380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe	395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro	410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr	425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu	440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gacacctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctggt gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50  
 cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100  
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150  
 tggatgatag aattttatgc cccgtggtgc cctgcttgctc aaaatcttca 200  
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250  
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300  
 ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350  
 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtata 400  
 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450  
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500  
 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550  
 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600  
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650  
 accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700  
 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatggt 750  
 tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800  
 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850  
 cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900  
 aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950  
 ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

acataaaaagc actaggtata caagtttgaa atatgattta agcacagtat 1050  
 gatgggttaa atagttctct aatttttgaa aaatcgtgcc aagcaataag 1100  
 atttatgtat atttgtttaa taataacctt tttcaagtct gagttttgaa 1150  
 aatttacatt tcccaagtat tgcattattg aggtatttaa gaagattatt 1200  
 ttagagaaaa atatttctca ttgatataa ttttctctg tttcactgtg 1250  
 tgaaaaaaag aagatatttc ccataaatgg gaagtttgcc cattgtctca 1300  
 agaaatgtgt atttcagtga caatttcgtg gtcttttttag aggtatattc 1350  
 caaaatttcc ttgtattttt aggttatgca actaataaaa actaccttac 1400  
 attaatattt tacagttttc tacacatggg aatacaggat atgctactga 1450  
 tttaggaagt ttttaagttc atgggtattct cttgattcca acaaagtttg 1500  
 attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550  
 caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600  
 tatttttttg ttgtttcaaa ctgaagtta ctgagagatc catcaaattg 1650  
 aacaatctgt tgtaatttaa aattttggcc acttttttca gattttacat 1700  
 cattcttgct gaacttcaac ttgaaattgt ttttttttc tttttggatg 1750  
 tgaagggtgaa cattctctgat tttgtctga tgtgaaaaag ccttggtatt 1800  
 ttacattttg aaaattcaaa gaagcttaat ataaaagttt gcattctact 1850  
 caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900  
 atacagaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950  
 aaataataac atttttatat tttttaaaag acaaacttca tattatcctg 2000  
 tgttctttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050  
 gtaggatgga acattttagt gtatttttac tccttaaaga gctagaatac 2100  
 atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150  
 ctgaccatta cgtagtagac aatttctgta atgtccctt ctttctaggc 2200  
 tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250  
 ttcttttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300  
 tttggatgtg taacttgtga tgccttagaa aaatatecta agcacaaaat 2350



215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys	Val Glu Glu Glu Gln Glu	
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu	Glu Ala Glu Ser Lys Glu	
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn	Ala Ile Arg Gln Arg Ser	
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys	Ser	
275	280	

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcggtaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgctacaaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgctct gcaggactca gctgcagggt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgcccgaag cctgatgaga cttcaggaca catacaggct 600

ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggcccgtc ggctacaat 700

gaaggggact attatcatat ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800  
 acctcageta tgctgtcttc cagttgggtg atctgcaccg tgccttgagg 850  
 ctcacccgcc gcctgtcttc ccttgacca agccacgaac gagctggagg 900  
 gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950  
 taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000  
 aggctgtgag actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050  
 tggggagggt gtcaaactga cccccgtag acagaagagg cttttctgta 1100  
 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150  
 gaggaggacg agtgggacag cccgcacatc gtcaggtagt acgatgtcat 1200  
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250  
 cagagccac cgttcgtgat cccaagacag gagtcctcac tgcgccagc 1300  
 taccgggttt ccaaaagctc ctggctagag gaagatgatg acctgttgt 1350  
 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400  
 ctgcagaatt gttacagggt gcaaattatg gaggggagg acagtatgaa 1450  
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaacaga 1500  
 ggggaatagg tttagcgagt ttcttaacta catgagtgat gtagaagctg 1550  
 gtggtgccac cgtcttcctt gatctggggg ctgcaatttg gcctaagaag 1600  
 ggtacagctg tgttctggta caacctcttg cggagcgggg aaggtagta 1650  
 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700  
 ccaataagtg gttccatgaa cgaggacagg agttcttgag accttggtga 1750  
 tcaacagaag ttgactgaca tccttttctg tccttcccct tctggtcct 1800  
 tcagcccatg tcaacgtgac agacacctt gtatgttcct ttgtatgttc 1850  
 ctatcaggct gatttttgga gaaatgaatg tttgtctgga gcagaggagg 1900  
 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950  
 gcctgtgcc tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000  
 gttagctgtc tagcgcttag caaggctcct ttgtacctca ggtgttttag 2050  
 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val	1	5	10	15
Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met	20	25	30	
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120	
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135	
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150	
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
 500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
 515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
 530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336  
acactcagca ttgcctggta cttg 24

<210> 337  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 337  
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338  
<211> 2789

<212> DNA  
<213> Homo Sapien

<400> 338  
gcagtattga gttttacttc ctctctttt tagtggaaga cagaccataa 50  
tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100  
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150  
agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200  
gctctgtctt tggcctcatt gaccccaggt tctctggtta aaactgaaag 250  
cctactactg gcctggtgcc catcaatcca ttgatccttg aggctgtgcc 300  
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350  
ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400  
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450  
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500  
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550  
cccctactac agggacccca acaagcccta caagaagggtg ctgaggactc 600  
ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650  
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700  
ggtggcccat cacttcccctc ggttactcta cttcactggg cagcgggggg 750  
cccgggctcc agcagggatg caggtggtgt ctcattgggga tgagcggccc 800

gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850  
 cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900  
 cccgcctggc agcccttgct ggccacotca gcatcaacca agacctgtac 950  
 ttaggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000  
 tcatgggggc tttggctacc tgttgtcacg gagtctcctg cttcgtctgc 1050  
 ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100  
 gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150  
 acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200  
 accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250  
 cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300  
 tctggagttg gagcgggctt acagtgaat agaacaactg caggctcaga 1350  
 tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400  
 cccgttgggc tccttgcctc ttccacacca cactctcgct ttgaggtgct 1450  
 gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500  
 ctcccaagtg cccactacag ggggctagca gggcggacgt gggatgatgcg 1550  
 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600  
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650  
 ggggcatgga gtacaccctg gacctgctgt tggaatgtgt gacacagcgt 1700  
 gggcaccggc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750  
 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800  
 agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850  
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagAAC atgcattgct 1900  
 caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950  
 acccatttct tggggtgaag gctgcagcag cggagttaga gcgacggtac 2000  
 cctgggacga ggctggcctg gctcgtctgt cgagcagagg ccccttccca 2050  
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
 tgtcgcacga atgcatctc tggtggcag gccttcttc cagtccattt 2200  
 ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccagggcccc 2250  
 cgggggctgg cctgacccc cctccccc cttggtgctga cccctcccg 2300  
 ggggctccta taggggggag atttgaccgg caggcttctg cggagggctg 2350  
 cttctacaac gctgactacc tggcgggccg agcccggtg gcaggatgaac 2400  
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450  
 gttttcctcc ggttctcagg gctccacctc tttcgggccg tagagccagg 2500  
 gctggtgcag aagttctccc tgcgagactg cagccacagg ctcatgaag 2550  
 aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
 gccgcctgg gggccctaac ctcattacct ttcctttgtc tgcctcagcc 2700  
 ccaggaaggg caaggcaaga tgggtggacag atagagaatt gttgctgtat 2750  
 tttttaaata tgaatatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1				5					10					15

Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
			20						25					30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95										100					105				
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val					
				110					115					120					
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr					
				125					130					135					
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser					
				140					145					150					
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg					
				155					160					165					
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile					
				170					175					180					
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu					
				185					190					195					
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala					
				200					205					210					
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly					
				215					220					225					
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg					
				230					235					240					
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro					
				245					250					255					
Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly					
				260					265					270					
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu					
				275					280					285					
Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu					
				290					295					300					
Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr					
				305					310					315					
Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr					
				320					325					330					
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val					
				335					340					345					
Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu					
				350					355					360					

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp			
															365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala			
															380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp			
															395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro			
															410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg			
															425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu			
															440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg			
															455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met			
															470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu			
															485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe			
															500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu			
															515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp			
															530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg			
															545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala			
															560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro			
															575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly			
															590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp			
															605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu			
															620	625	630

Ser	Pro	Gln	Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp	
				635					640					645	
Pro	Pro	Ser	Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile	
				650					655					660	
Gly	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr	
				665					670					675	
Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu	
				680					685					690	
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met	
				695					700					705	
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val	
				710					715					720	
Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro	
				725					730					735	
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu	
				740					745					750	
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu	
				755					760					765	
Gln	Glu	Gln	Ala	Asn	Ser	Thr									
				770											

&lt;210&gt; 340

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 340

```

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50
tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100
ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

```

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450  
 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
 ttccttgcaac gcccactac gtttgcctac attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgccct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900  
 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 ggtttttotta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tgttgcatt atttgtagta 1100  
 gtaactacat atccaataca gctgtatggt tctttttctt ttctaatttg 1150  
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200  
 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaag 1250  
 aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300  
 atgtgataaa ttctaataa tgaacattag aaatctgtgg ggcacatatt 1350  
 tttgctgatt ggtaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaaa 1500  
 gttccaatgg atttgcttc tcaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

&lt;400&gt; 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly	1	5	10	15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	230	235	240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	245	250	255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys				

	260		265		270									
Cys	Ser	Asp	Met	Ala	Val	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Asn	Gln
			275						280					285
Met	His	Val	Met	Met	Tyr	Gly	Val	Tyr	Arg	Leu	Arg	Ala	Phe	Gly
			290						295					300
His	Ile	Phe	Asn	Asp	Ala	Leu	Val	Phe	Leu	Pro	Pro	Asn	Gly	Ser
			305						310					315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctgggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaagtc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 350  
 ggattctaatacgcactcactatagggcgccgatgtccactggggctac 48  
  
 <210> 351  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 351  
 ctatgaaattaacctcactaaagggacgaggaagatggcggatggc 48  
  
 <210> 352  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 352  
 ggattctaatacgcactcactatagggcaccacgcgtccggtgctt 47  
  
 <210> 353  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 353  
 ctatgaaattaacctcactaaagggacggggacaccacggaccaga 48  
  
 <210> 354  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 354  
 ggattctaatacgcactcactatagggcttgctgcggttttgttcctg 48  
  
 <210> 355  
 <211> 48

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 355  
 ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48  
  
 <210> 356  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 356  
 ggatttcta atcgactcact atagggcgga tcctggccgg cctctg 46  
  
 <210> 357  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 357  
 ctatgaaatt aaccctcact aaaggagcc cgggcatggt ctcagtta 48  
  
 <210> 358  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 358  
 ggatttcta atcgactcact atagggcgga aagatggcga ggaggag 47  
  
 <210> 359  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 359  
 ctatgaaatt aaccctcact aaaggaccca aggccacaaa cggaaatc 48

<210> 360  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 360  
ggattctaatac gactcact atagggctgt gctttcattc tgccagta 48

<210> 361  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 361  
ctatgaaatt aaccctcact aaagggaggg tacaattaag ggggtggat 48

<210> 362  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 362  
ggattctaatac gactcact atagggcccg cctcgctcct gctcctg 47

<210> 363  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 363  
ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48

<210> 364  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaatacgcactcactatagggccccctctgccttcctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaattaacccctcactaaagggagtggtggccgcgattatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaatacgcactcactatagggcgcatcgatggcagcgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaattaacccctcactaaaggacagacggggcagagggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaatacgcactcactatagggccagaggcggtgaggagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatt acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaatac gactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaagag 50

agggagggag agaaaaagag agagagagaa aaaaaaaccc aaagagagag 100

aaaaaatgaa ttcatctaaa tcctctgaaa cacaatgcac agagagagga 150

tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200

atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350

gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400

tttctctggg gttaagttaa aagaactgct cagccatggg ggctcacctg 450

gtgggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550

agtggcaatg ggtggacggc acacctttga caaagtctct gagcttcttg 600

gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc tttaagaaca gaaggcacia ctcaaattgtg taaagaagga 800  
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgctc 850  
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900  
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly	1	5	10	15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro	20	25	30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr	35	40	45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
                                   185                                  190                                  195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
                                   200                                  205                                  210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
                                   215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagcttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagattttg aggacagcca cctcca 26

<210> 382  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 382  
ggccttgacg acaaccgt 18

<210> 383  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 383  
cagactgagg gagatccgag a 21

<210> 384  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 384  
cagctgcccct tccccaacca 20

<210> 385  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 385  
catcaagcgc ctctacca 18

<210> 386  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386

cacaaactcg aactgcttct g 21

<210> 387

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

gggccatcac agctccct 18

<210> 388

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gggatgtggt gaacacagaa ca 22

<210> 389

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 389

tgccagctgc atgctgccag tt 22

<210> 390

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
gaagagcaca gctgcagatc c 21

<210> 397  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
gaggtgtcct ggcttttggtta gt 22

<210> 398  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 398  
cctctggcgc cccactcaa 20

<210> 399  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 399  
ccaggagagc tggcgatg 18

<210> 400  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 400  
gcaaattcag ggctcactag aga 23

<210> 401  
<211> 29

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 401  
cacagagcat ttgtccatca gcagttcag 29

<210> 402  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 402  
ggcagagact tccagtcact ga 22

<210> 403  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 403  
gccaaggggtg gtgtagata gg 22

<210> 404  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
caggccccct tgatctgtac ccca 24

<210> 405  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 405  
gggacgtgct tctacaagaa cag 23

<210> 406  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
caggcttaca atggttatgat cagaca 26

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
tattcagagt tttccattgg cagtgccagt t 31

<210> 408  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
tctacatcag cctctctgcg c 21

<210> 409  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 409  
cgatcttctc caccaggag cgg 23

<210> 410  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 410

gccaggcctc acattcgt 18

<210> 411

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

ctccctgaat ggcagcctga gca 23

<210> 412

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

aggtgtttat taaggccta cgct 24

<210> 413

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cagagcagag ggtgccttg 19

<210> 414

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 414

tggcggagtc ccctcttggc t 21

<210> 415

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 420  
 tgtctgcctc agccccagga agg 23

<210> 421  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 421  
 tctgtccacc atcttgctt g 21

<210> 422  
 <211> 3554  
 <212> DNA  
 <213> Homo Sapien

<400> 422  
 gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50  
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100  
 cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150  
 tcaaatccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200  
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250  
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300  
 ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350  
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400  
 cgttgctcga aatgaccgca aggaaattga tgagatttg atcgagttaa 450  
 ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500  
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550  
 ccggcctcac tacagctggg atcgcaatga tgtaccactg cccacggatt 600  
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650  
 acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700  
 ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg ggggggttctg 800  
 gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850  
 cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900  
 acccagggaa accagatgga gttaactaca tccgcaactga cgaggagggc 950  
 gacttcagac acaagtcatc gtttgtgatc tgagaccgcg ggtgtggctg 1000  
 agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050  
 ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100  
 ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150  
 catgaataga agaattttcc tcaagatgga cccggtaaat ataaccacaa 1200  
 ggaagcgaaa ctgggtgcgt tcaactgagt gggttcctaa tctgtttctg 1250  
 gcctgattcc cgcattgagta ttagggatgat cttaaagagt ttgctcacgt 1300  
 aaacgcccgt gctgggccct gtgaagccag catgttcacc actggctcgtt 1350  
 cagcagccac gacagcacca tgtgagatgg cgagggtggct ggacagcacc 1400  
 agcagcgcac cccggcgagg acccagaaaa ggcttcttac acagcagcct 1450  
 tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500  
 tgatcggtgt tgcagtgtcc attgtggaga agcttttttg atcagcattt 1550  
 tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600  
 cttgcctgag gaaccctgct tgtccaacag ggtgtcagga tttaaggaaa 1650  
 accttcgtct taggctaagt ctgaaatggt actgaaatat gcttttctat 1700  
 gggctctggt tattttataa aattttacat ctaaattttt gctaaggatg 1750  
 tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800  
 catacaatgt taaataacct atttttttta aaaagttcaa cttaaggtag 1850  
 aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900  
 ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950  
 cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000  
 agaccatagt tgcttaggaa accttttaaa attccagtta agcaatggtg 2050

aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100  
 gcctcttcct gagatgacta ggacagtctg taccagagg ccacccagaa 2150  
 gccctcagat gtacatacac agatgccagt cagctcctgg ggttgogcca 2200  
 ggcgcccccg ctctagctca ctgttgctc gctgtctgcc aggaggccct 2250  
 gccatccttg ggccctggca gtggctgtgt cccagtgage tttactcacg 2300  
 tggcccttgc ttcacccagc acagctctca ggtgggcact gcagggacac 2350  
 tgggtgtcttc catgtagcgt cccagctttg ggctcctgta acagacctct 2400  
 ttttggttat ggatggctca caaaataggg cccccaatgc tatttttttt 2450  
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500  
 tgcgaaatca agtctgtcaa gtacaataac attttttaaaa gaaaatggat 2550  
 cccactgttc ctctttgcc aagagaaagc acccagacgc cacaggctct 2600  
 gtcgcatttc aaaacaaacc atgatggagt ggcgccagc ccagcctttt 2650  
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaaag 2700  
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750  
 atccgccgga gacactgtc ccatttgtgg ggggacatta gcaacatcac 2800  
 tcagaagcct gtgttcttca agagcagggtg ttctcagcct cacatgccct 2850  
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900  
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcaccttgt 2950  
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000  
 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050  
 tgccgcaggc cgcctggcag aggcaggaaa tgctccagca gtggctcagt 3100  
 gctccctggg gtctgtgca tggcatcctg gatgcttagc atgcaagtgc 3150  
 cctccatcat tgccaccttg gtagagaggg atggctcccc accctcagcg 3200  
 ttggggattc acgctccagc ctcttcttgg gttgtcatag tgatagggtta 3250  
 gccttatttg cccctcttct tataacctaa aaccttctac actagtgcc 3300  
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350  
 gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450  
gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500  
caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550  
ccca 3554

<210> 423  
<211> 310  
<212> PRT  
<213> Homo Sapien

<400> 423  
Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu  
1 5 10 15  
Pro Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly  
20 25 30  
Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu  
35 40 45  
Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr  
50 55 60  
Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr  
65 70 75  
Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly  
80 85 90  
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val  
95 100 105  
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg  
110 115 120  
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val  
125 130 135  
Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val  
140 145 150  
Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly  
155 160 165  
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu  
170 175 180  
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe  
185 190 195

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
				200					205					210
Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					

200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310